Family TD - 1

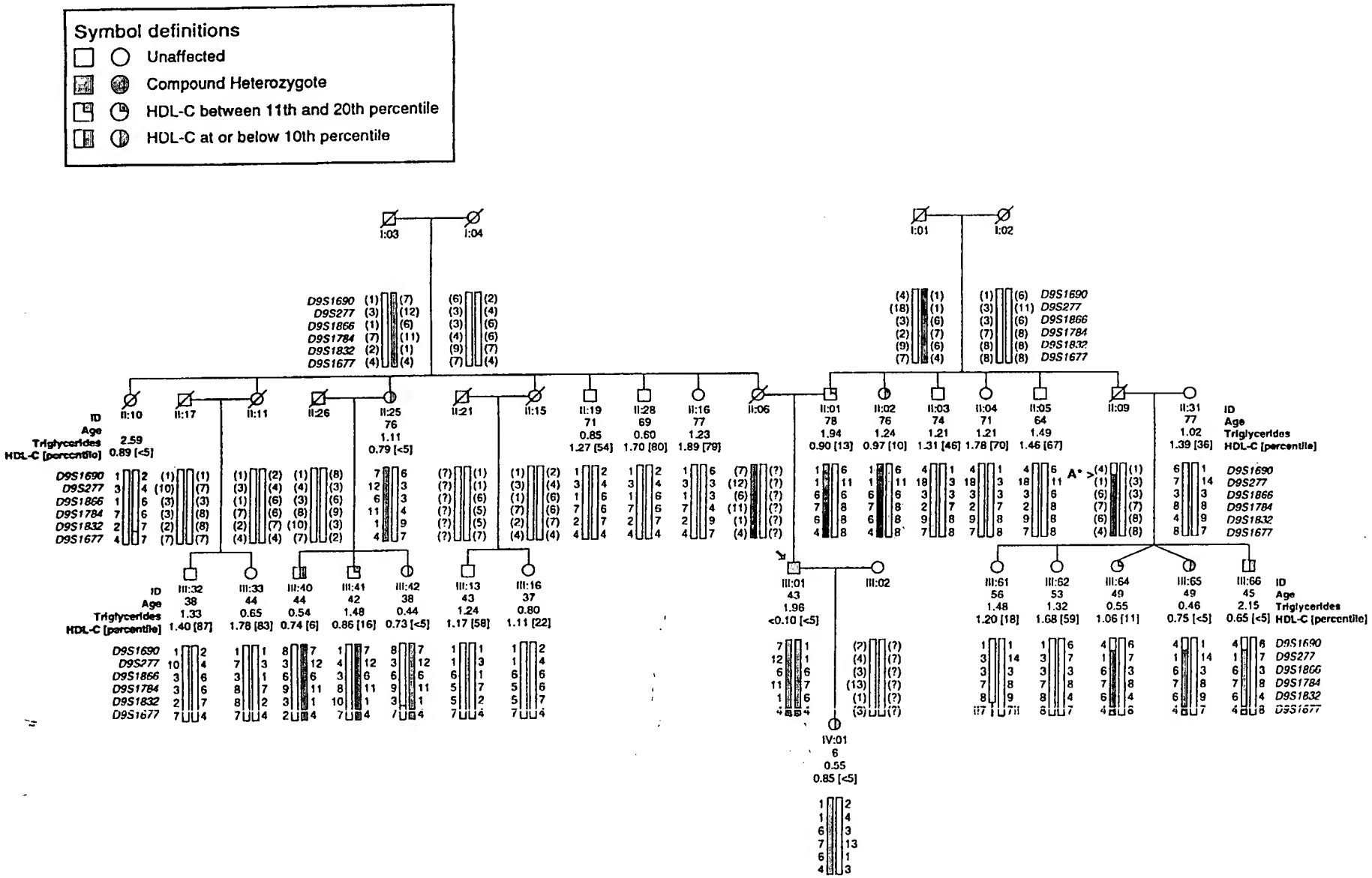


Fig. 1A

DUSTED EDITED

Family TD - 2

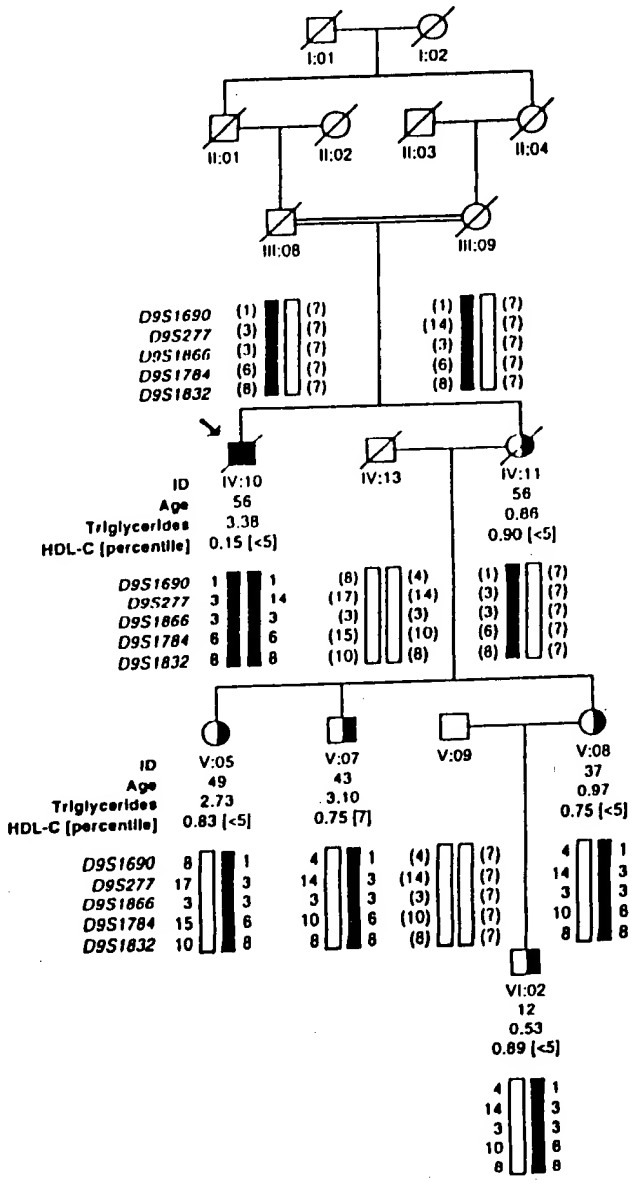


Fig. 1B

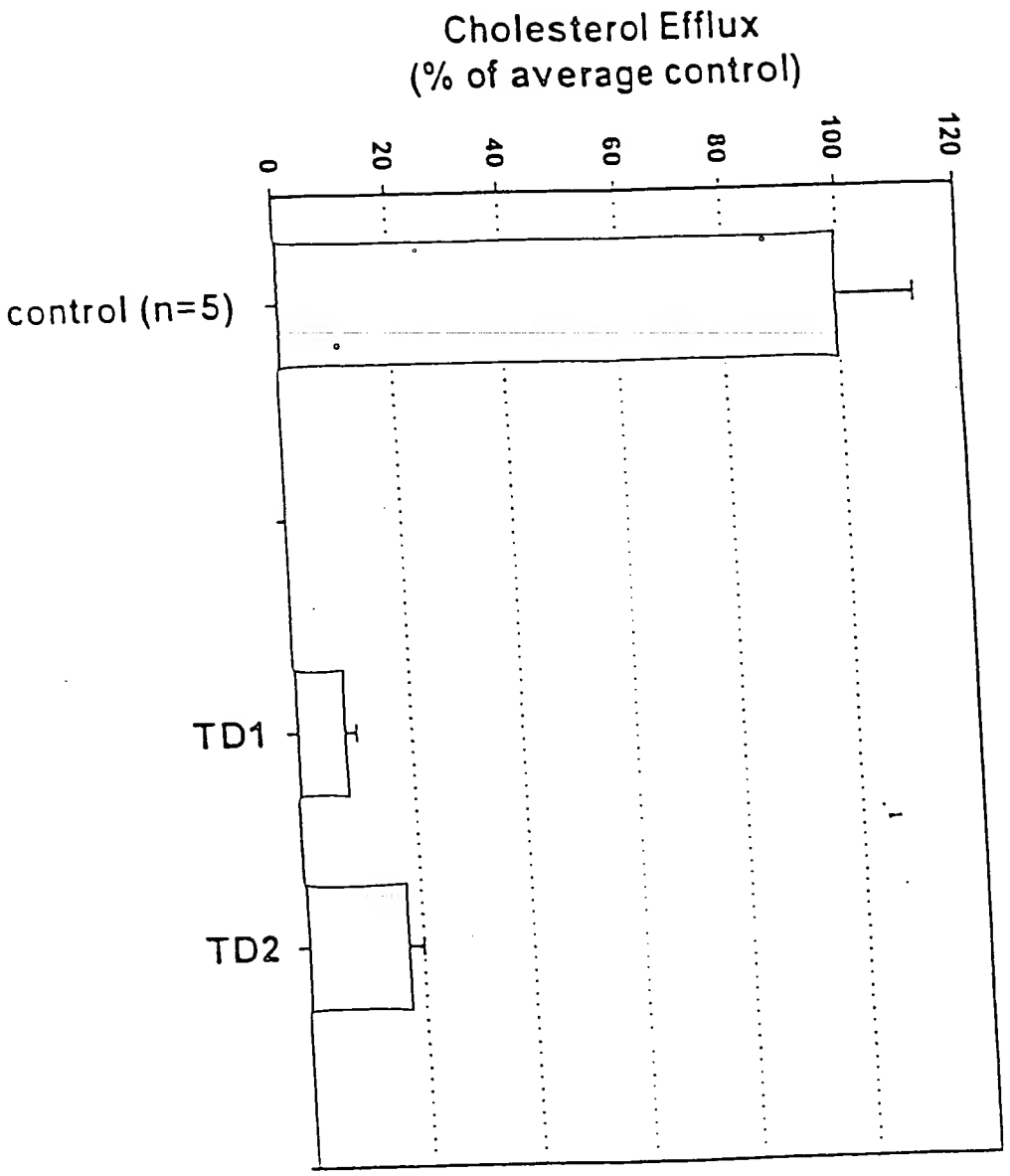

Cholesterol Efflux
(% of average control)
0
20
40
60
80
100
120
control (n=5)
TD1
TD2

Fig. 1C

Fig. 2A

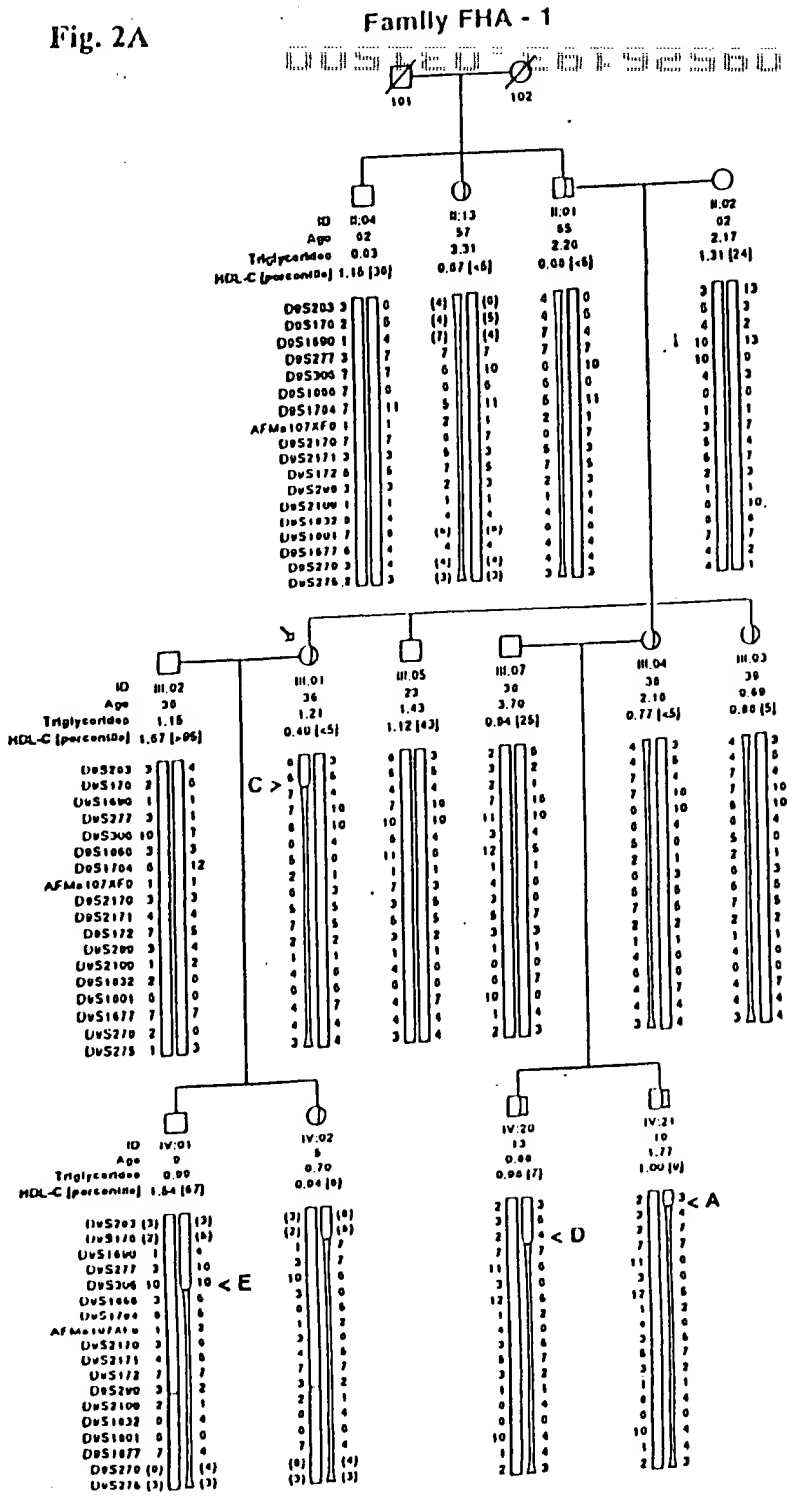
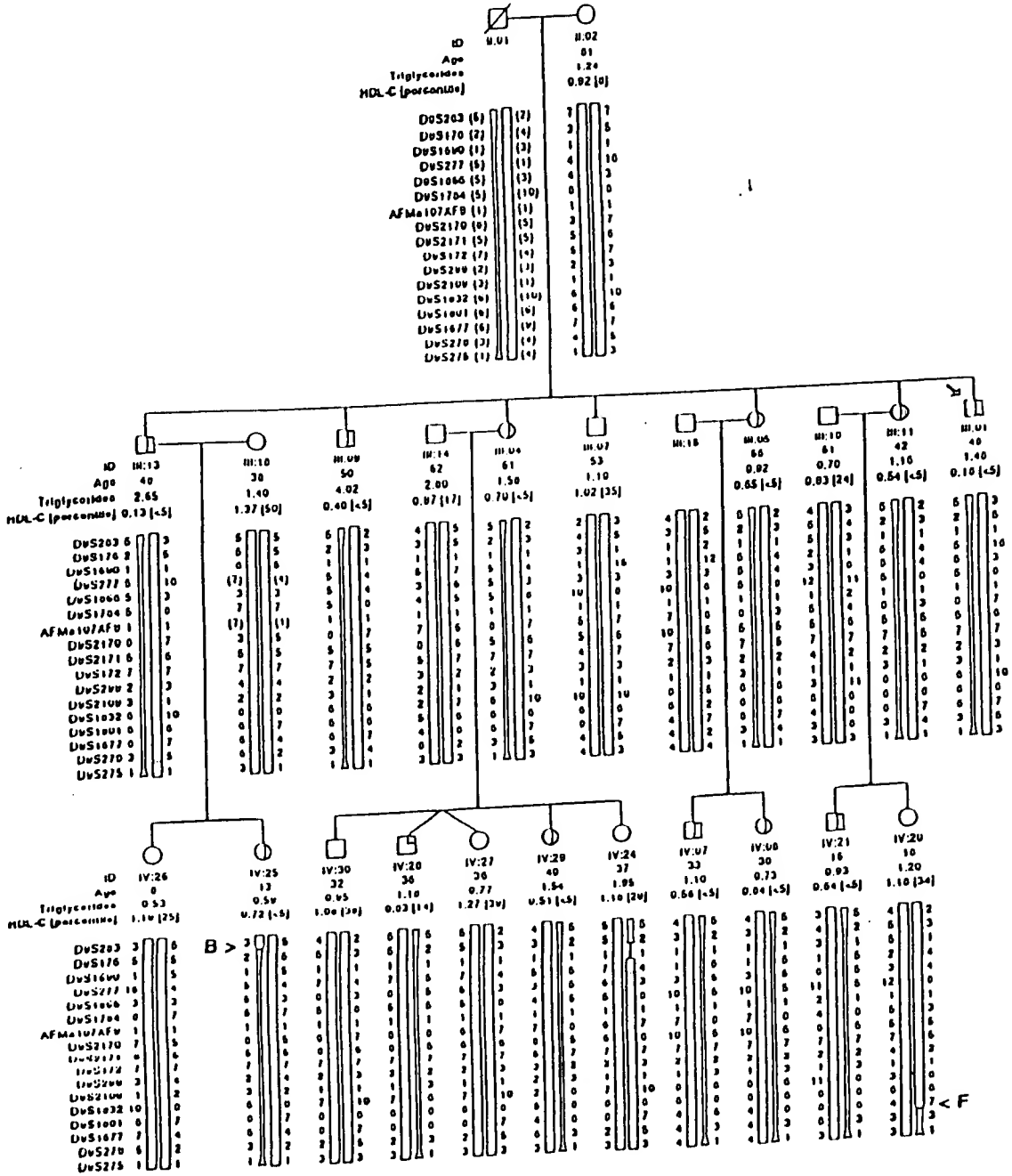

Family FHA - 1
I:01
I:02
II:04
II:13
II:01
II:02
III:02
III:01
III:05
III:07
III:04
III:03
IV:01
IV:02
IV:20
IV:21
C >
< E
< D
< A

Fig. 2B

Family FHA - 2



Family FHA - 3

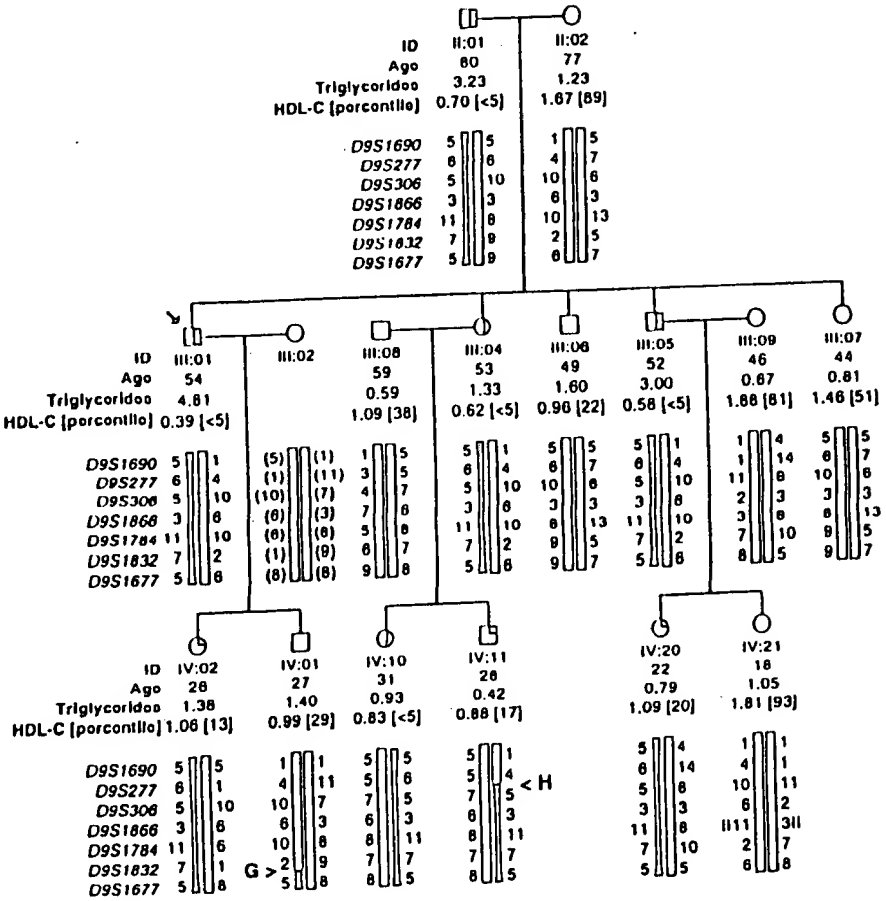
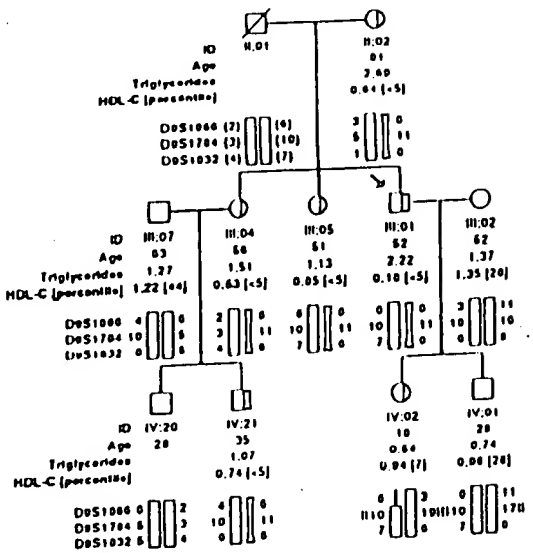


Fig. 2C

0054201 EP1921900

Fig. 2D

Family FHA - 4



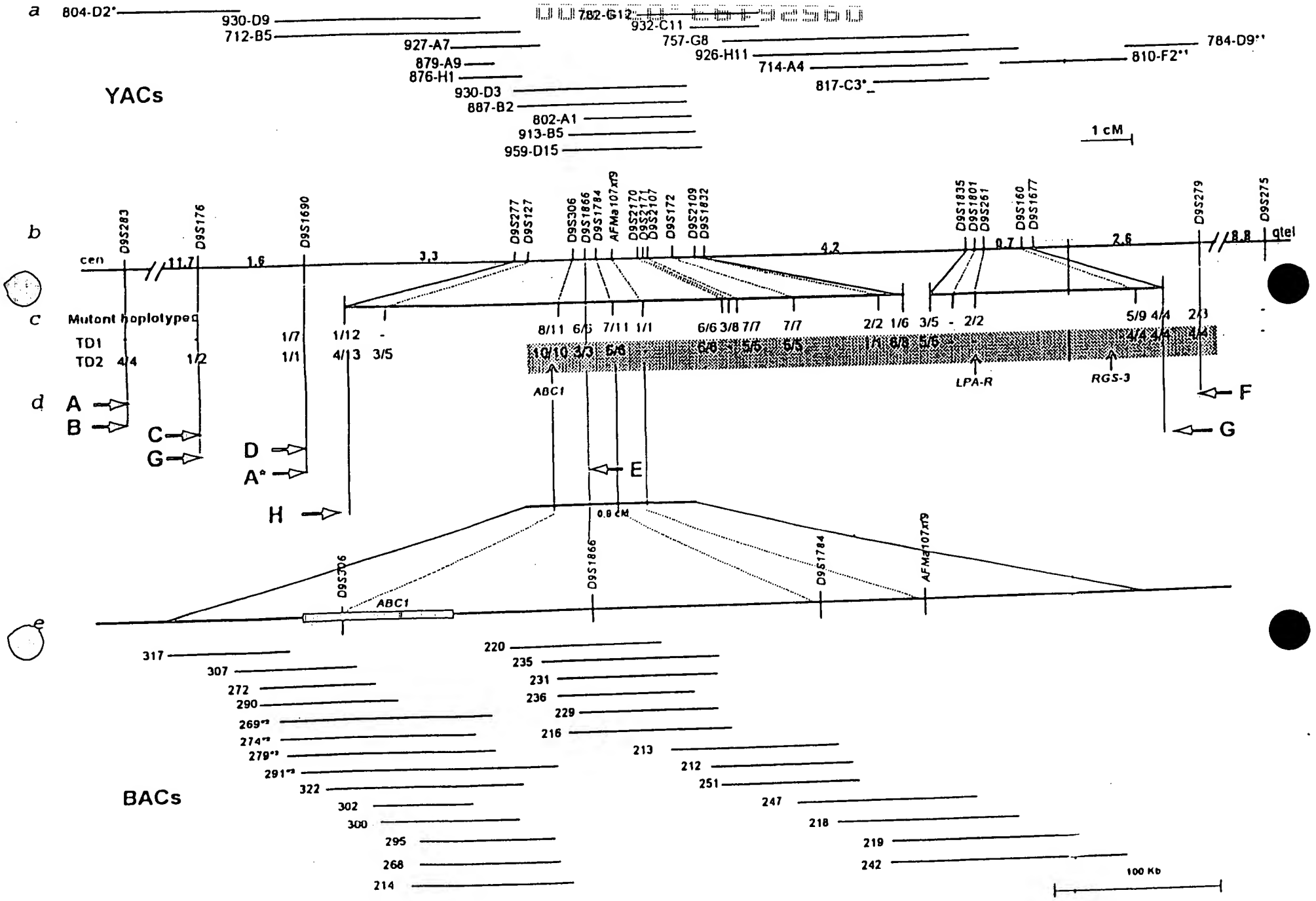

a
804-D2*
930-D9
712-B5
927-A7
879-A9
876-H1
930-D3
887-B2
802-A1
913-B5
959-D15
782-G12
932-C11
757-G8
926-H11
714-A4
817-C3*
784-D9**
810-F2**
YACs
1 cM
b
D9S283
D9S176
D9S1690
D9S277
D9S127
D9S306
D9S1866
D9S1784
AFMa107xf9
D9S2170
D9S2171
D9S2107
D9S172
D9S2109
D9S1832
D9S1835
D9S1801
D9S261
D9S160
D9S1677
D9S279
D9S275
cen
11.7
1.6
3.3
4.2
0.7
2.6
8.8
qtel
c
Mutant haplotypes
TD1
TD2
4/4
1/2
1/7
1/1
1/12
4/13
3/5
8/11
6/6
7/11
1/1
6/6
3/8
7/7
7/7
2/2
1/6
3/5
2/2
5/9
4/4
2/3
10/10
3/3
5/5
5/5
5/5
1/1
8/8
5/5
4/4
4/4
1/1
ABC1
LPA-R
RGS-3
d
A
B
C
G
D
A°
H
E
F
G
0.8 cM
D9S306
ABC1
D9S1866
D9S1784
AFMa107xf9
e
BACs
317
307
272
290
269**
274**
279**
291**
322
302
300
295
268
214
220
235
231
236
229
216
213
212
251
247
218
219
242
100 Kb

Fig. 3

DOSTED: 20020500

Exon 30 mutation:

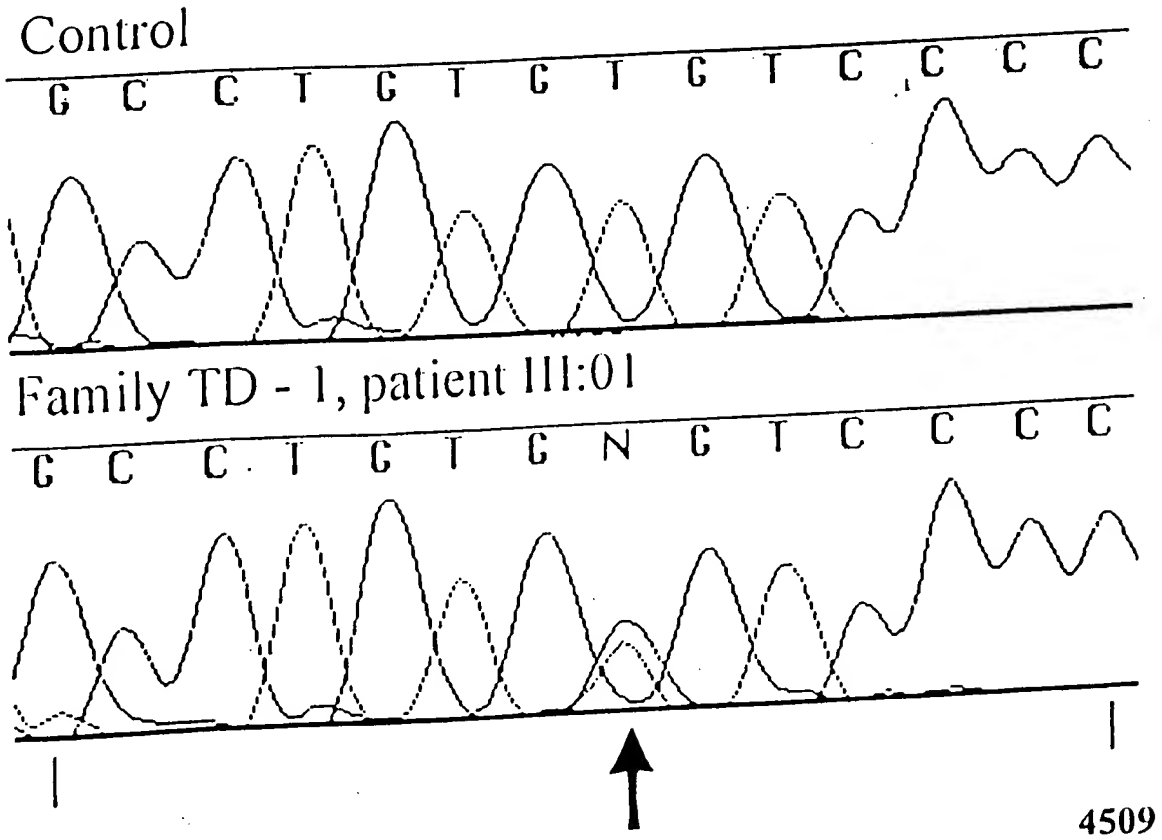


Fig. 4A

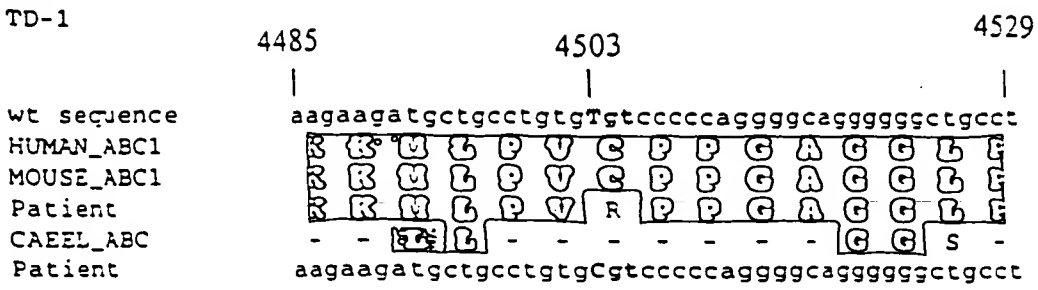

Exon 30
TD-1
4485
4503
4529
wt sequence
HUMAN_ABC1
MOUSE_ABC1
Patient
CAEEL_ABC
Patient
aagaagatgctgcctgtgTgtcccccaggggcaggggggctgcct
aagaagatgctgcctgtgCgtcccccaggggcaggggggctgcct

Fig. 4B

UNITED CONFIDENTIAL

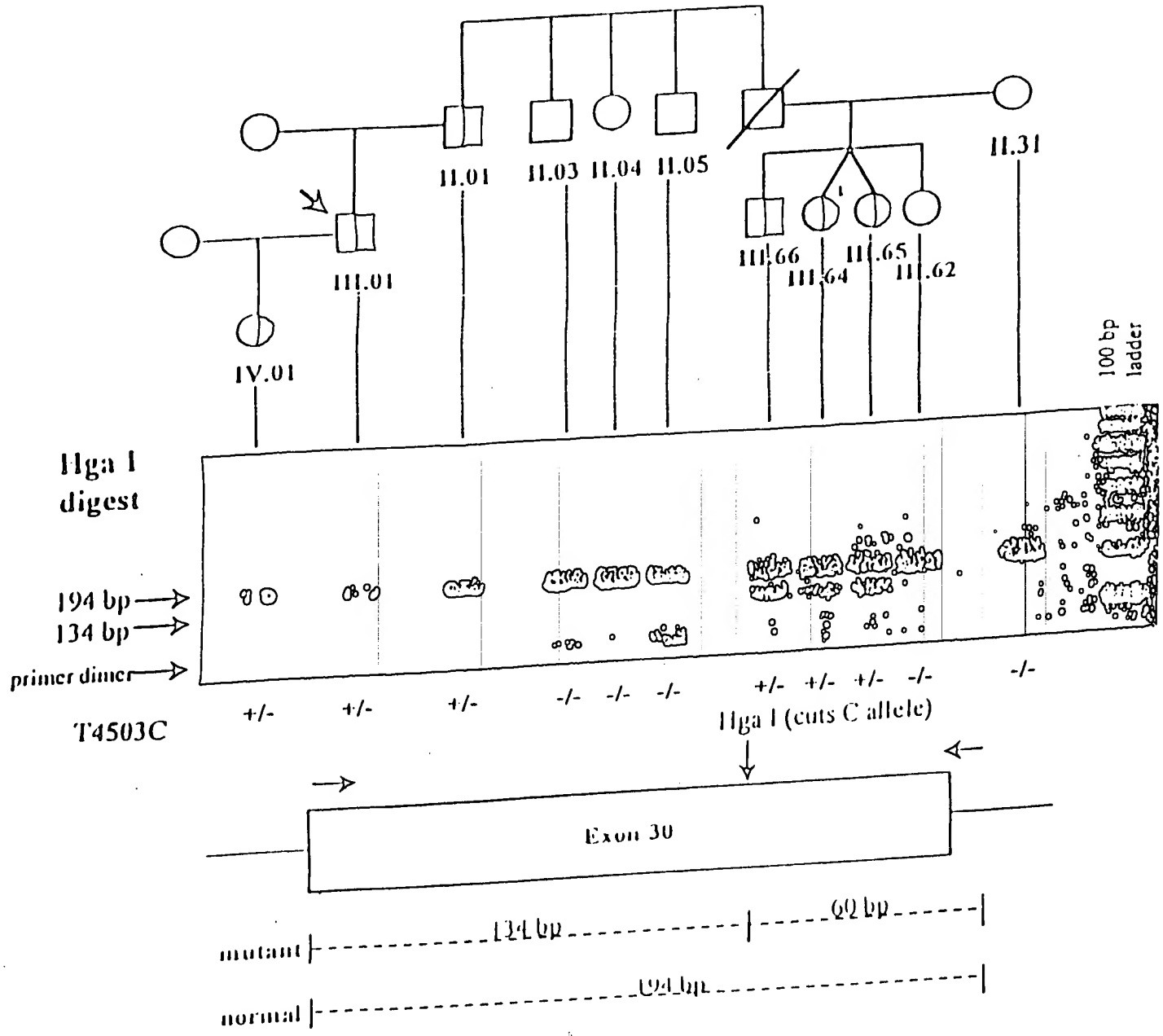


Fig. 4C

DUSTED 2019

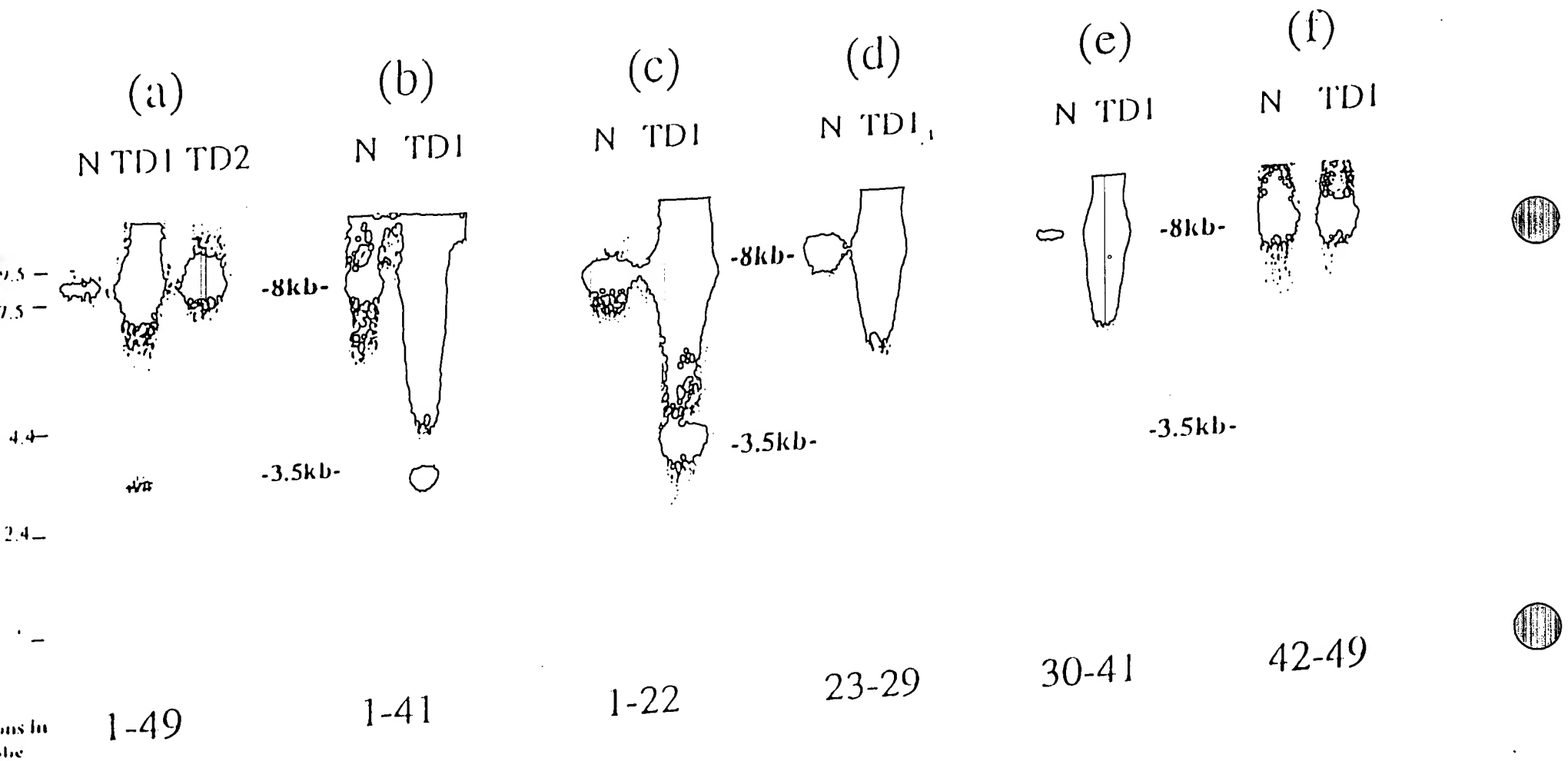


Fig. 4D

Exon 13 mutation:

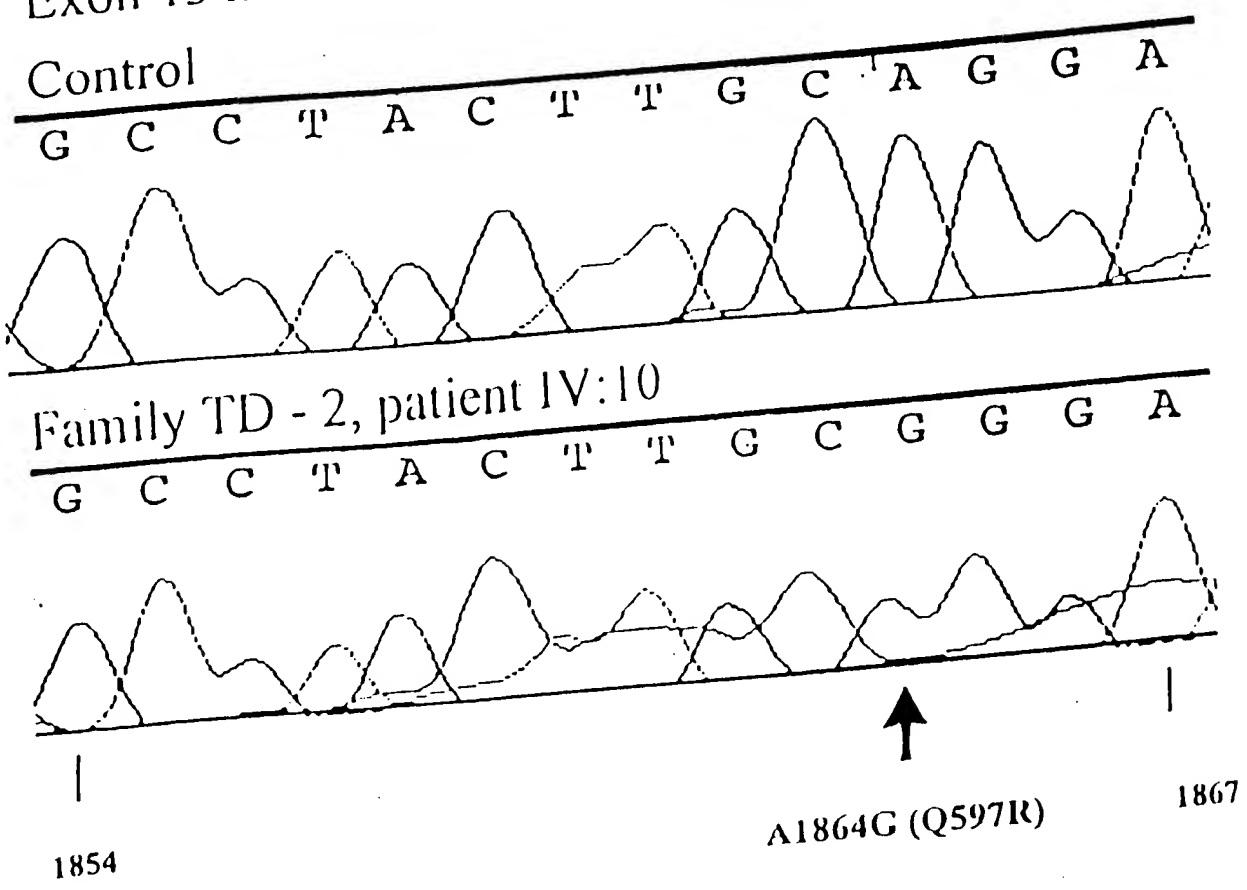


Fig. 5A

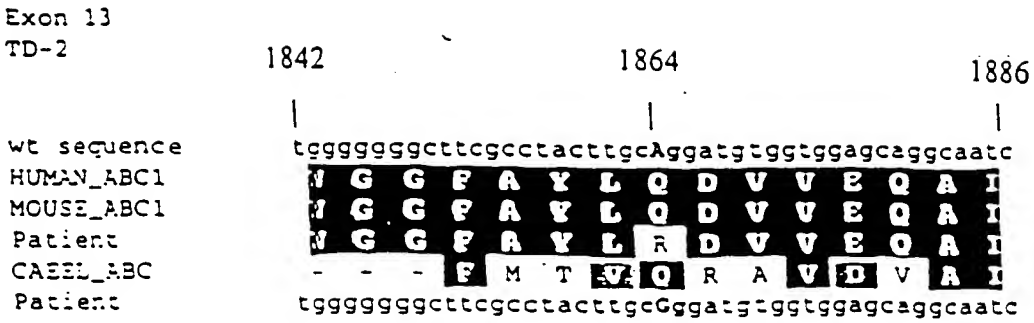

Exon 13
TD-2
1842
1864
1886
wt sequence
HUMAN_ABC1
MOUSE_ABC1
Patient
CAEEL_ABC
Patient
tgggggggcttcgcctacttgcAggatgtggtggagcaggcaatc
tgggggggcttcgcctacttgcGggatgtggtggagcaggcaatc

Fig. 5B

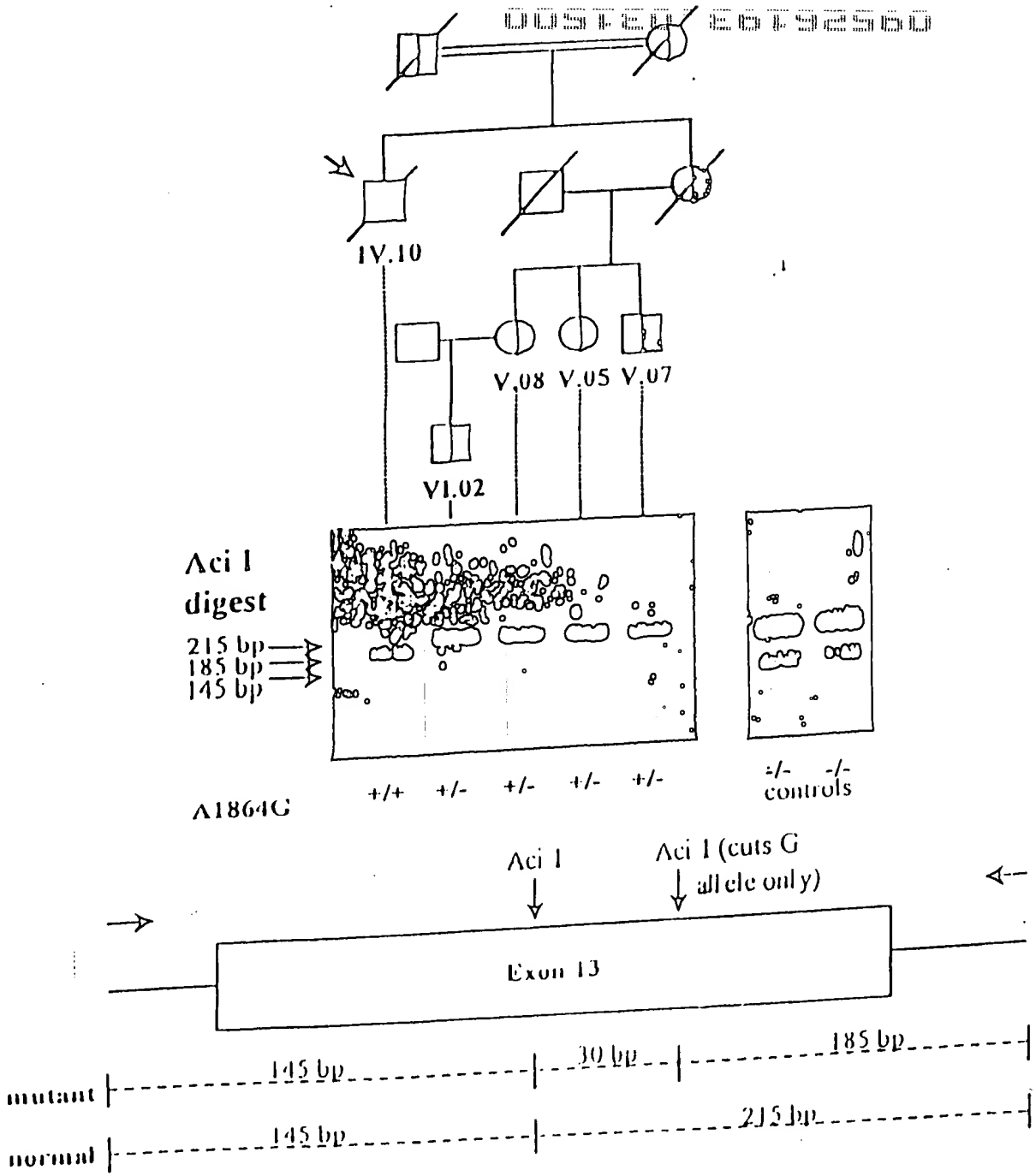

IV.10
V.08 V.05 V.07
VI.02
Aci I
digest
215 bp
185 bp
145 bp
A1864G
+/+ +/- +/- +/- +/-
-/- -/-
controls
Aci I
Aci I (cuts G
allele only)
Exon 13
mutant
145 bp
30 bp
185 bp
normal
145 bp
215 bp

Fig. 5C

Exon 14: FHA - 1, patient III:01

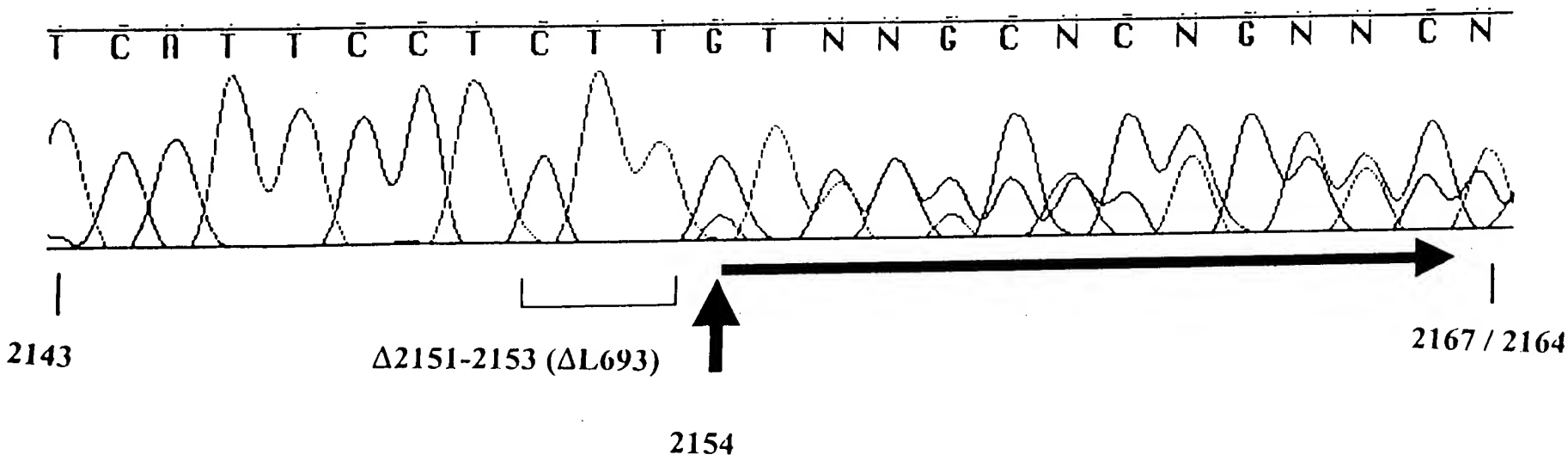


Fig. 6A

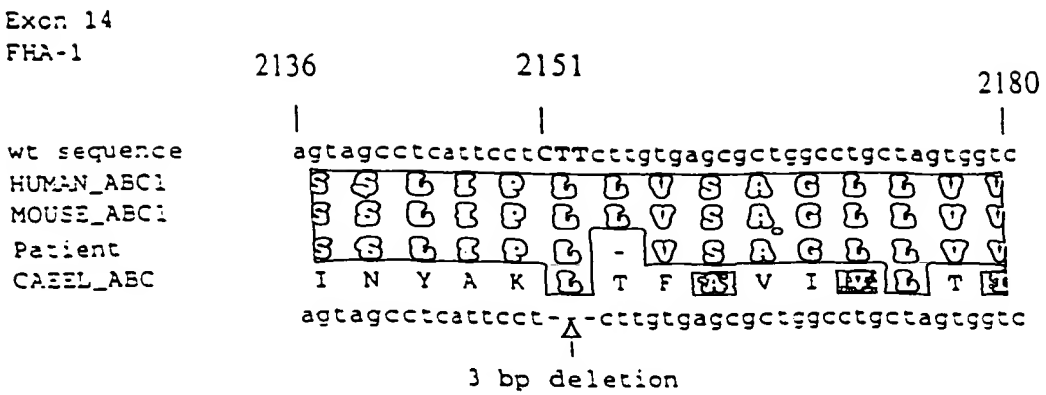

Exon 14
FHA-1
2136
2151
2180
wt sequence
agtagcctcattcctCTTcttgtgagcgctggcctgctagtggtc
HUMAN_ABC1
MOUSE_ABC1
Patient
CAEEL_ABC
I N Y A K
T F
V I
T
agtagcctcattcct-
-cttgtgagcgctggcctgctagtggtc
3 bp deletion

Fig. 6B

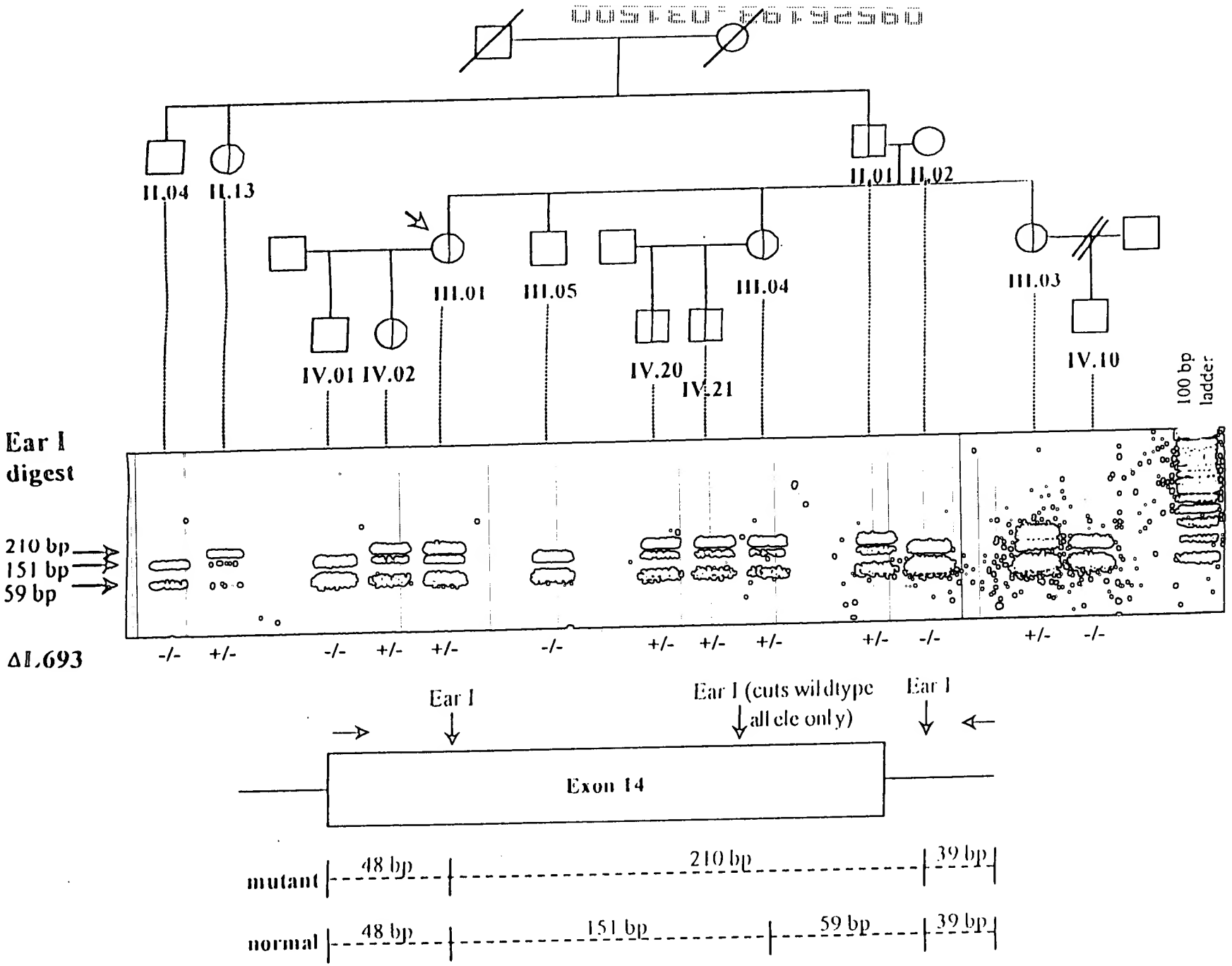

II.04
II.13
II.01
II.02
III.01
III.05
III.04
III.03
IV.01
IV.02
IV.20
IV.21
IV.10
100 bp ladder
Ear I digest
210 bp
151 bp
59 bp
ΔI.693
-/- +/- -/- +/- +/- -/- +/- +/- +/- +/- -/- +/- -/-
Ear I
Ear I (cuts wildtype allele only)
Ear I
Exon 14
mutant
48 bp
210 bp
39 bp
normal
48 bp
151 bp
59 bp
39 bp

Fig. 6C

DUSTED EDITED

Exon 41: FHA - 3, patient III:01

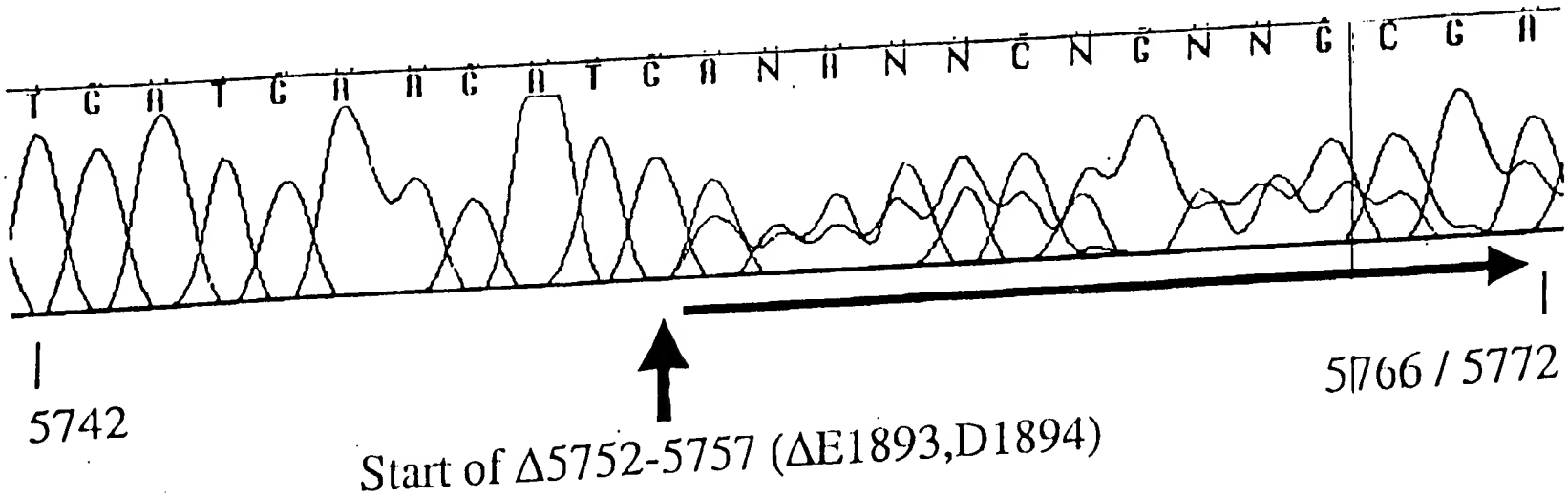


Fig. 6D

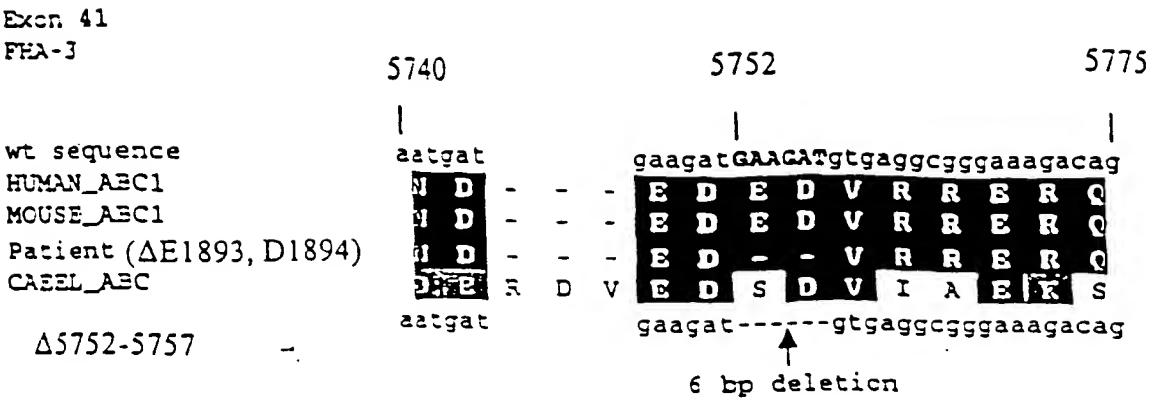

Exon 41
FHA-3
5740
5752
5775
wt sequence
HUMAN_ABC1
MOUSE_ABC1
Patient (ΔE1893, D1894)
CAEEL_ABC
Δ5752-5757
aatgat
gaagatGAACATgtgaggcgggaaagacag
N D - - - E D E D V R R E R Q
H D - - - E D E D V R R E R Q
Q D - - - E D - - V R R E R Q
D E R D V E D S D V I A E K S
aatgat
gaagat------gtgaggcgggaaagacag
6 bp deletion

Fig. 6E

DUSTED DEPOSED

Exon 48 mutation:

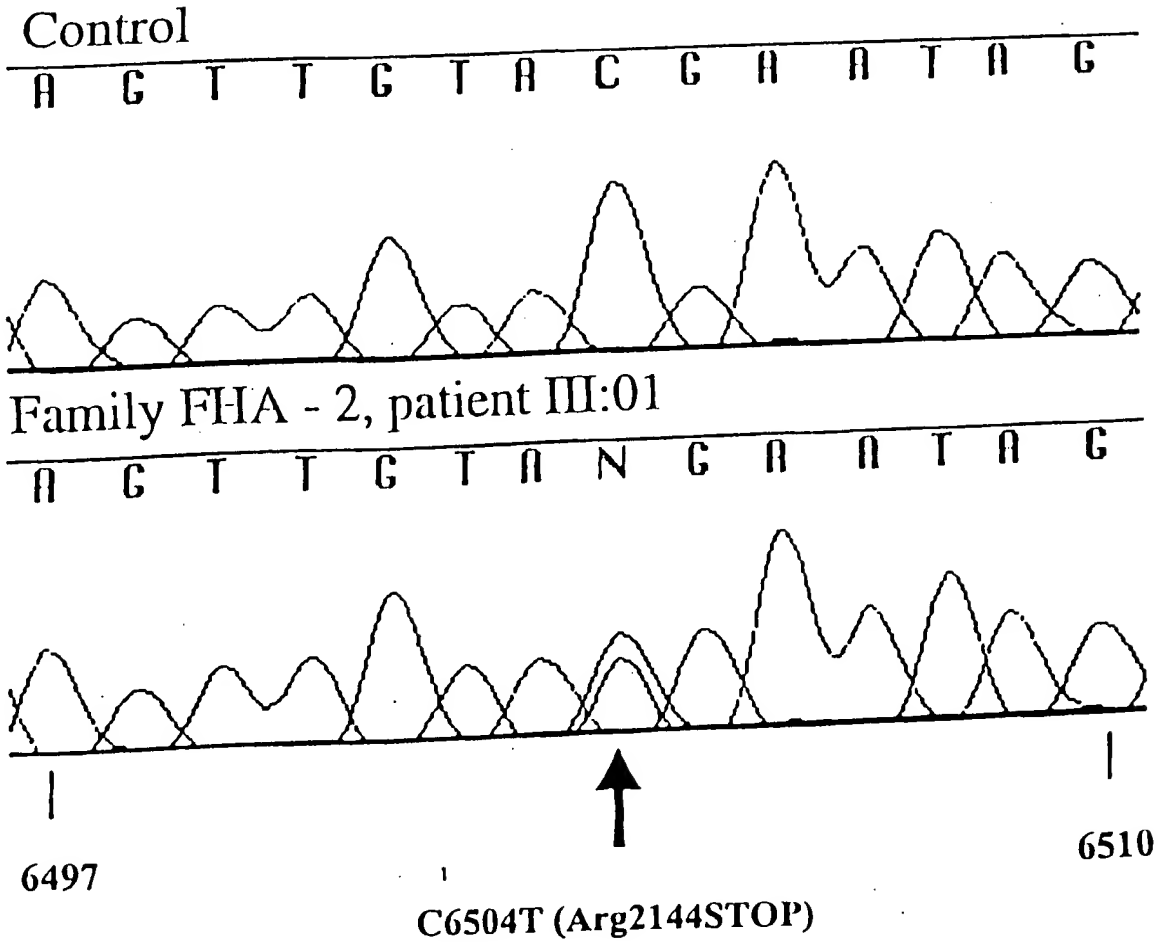


Fig. 6F

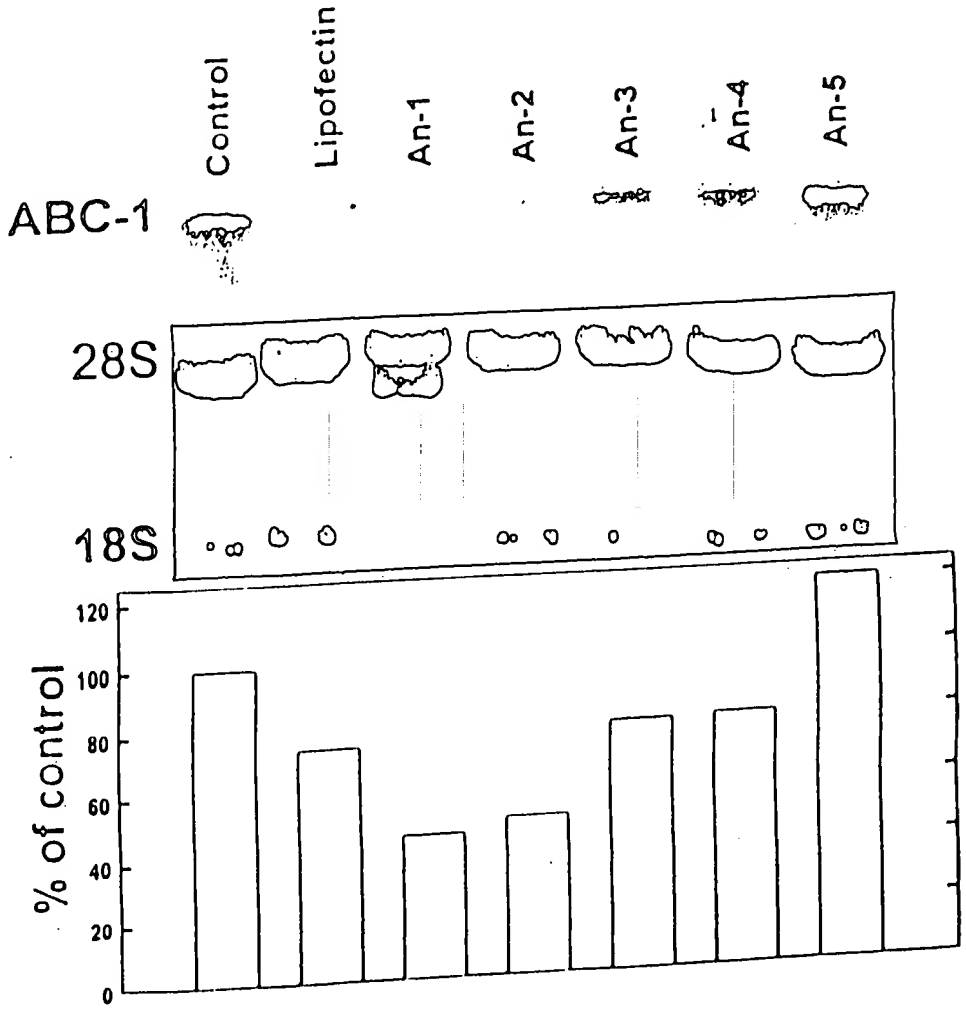

Control
Lipofectin
An-1
An-2
An-3
An-4
An-5
ABC-1
28S
18S
% of control
120
100
80
60
40
20
0

Fig. 7A

% Cholesterol Efflux
0
2
4
6
8
10
12
14
16
18
Control
Lipofectin
Antisense
Sense
FHA
TD
% Difference from Control
20
0
-20
-40
-60
-80
Control
Lipofectin
Antisense
Sense
FHA
TD

Fig. 7B

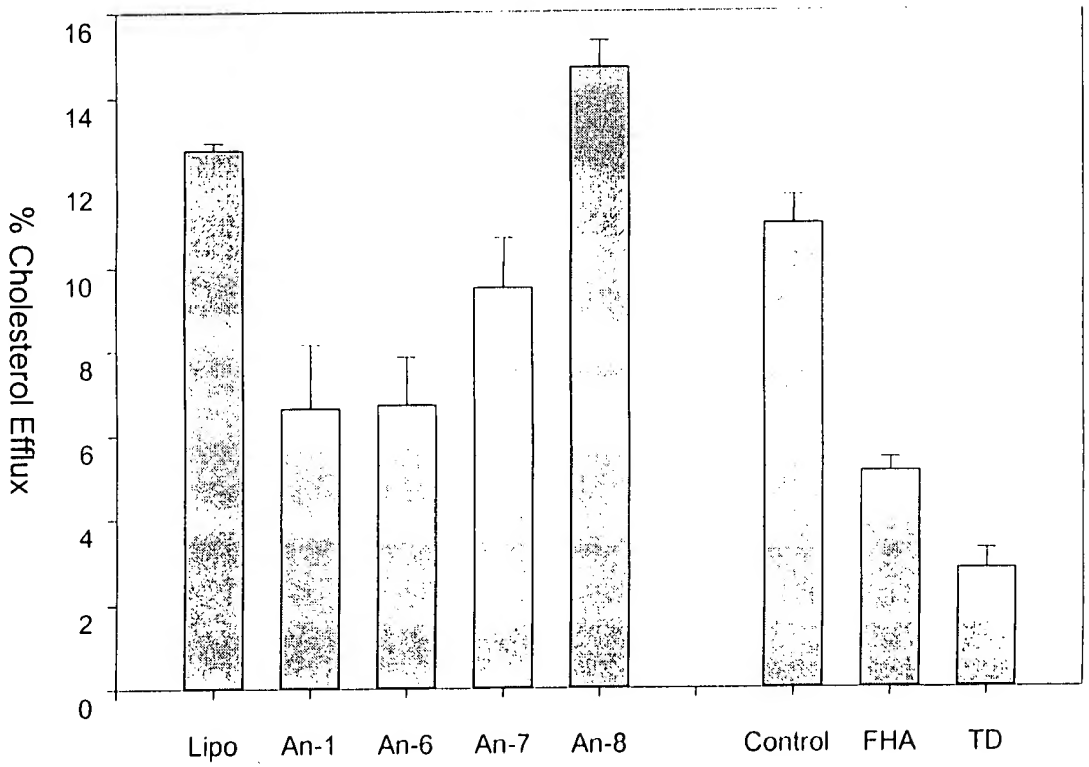

% Cholesterol Efflux
16
14
12
10
8
6
4
2
0
Lipo
An-1
An-6
An-7
An-8
Control
FHA
TD

Fig. 7C

SEQ ID NO: 1

MACWPQLRLLLWKNLTFRRRQTCQLLLEVAWPLFIFLILISVRLSYPPYEQHECHFPNKAMPSAGTLPWVQ
GIICNANNPCFRYPTPGEAPGVVGNFNKSIVARLFSDARRLLLYSQKDTSMKDMRKVLRTLQQIKKSSSNL
KLQDFLVDNETFSGFLYHNLSLPKSTVDKMLRADVILHKVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSE
LCGLPREKLAAAERVLRSNMDILKPILRTLNSTSPFPSKELAEATKTLLHSLGTLAQELFSMRSWSDMRQE
VMFLTNVNSSSSSTQIYQAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALFGGNGTEEDAETFYDNSTTPYC
NDLMKNLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTFQELAVFHDLEGMWEELSPKIWTF
MENSQEMDLVRMLLDSRDNDHFWEQQLDGLDWTAQDIVAFLAKHPEDVQSSNGSVYTWREAFNETNQAIRT
ISRFMECVNLNKLEPIATEVWLINKSMELLDERKFWAGIVFTGITPGSIELPHHVKYKIRMDIDNVERTNK
IKDGYWDPGPRADPFEDMRYVWGGFAYLQDVVEQAIIRVLTGTEKKTGVYMQQMPYPCYVDDIFLRVMSRS
MPLFMTLAWIYSVAVIIKGIVYEKEARLKETMRIMGLDNSILWFSWFISSLIPLLVSAGLLVVILKLGNLL
PYSDPSVVFVFLSVFAVVTILQCFLISTLFSRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFTLKIFASL
LSPVAFGFGCEYFALFEEQGIGVQWDNLFESPVEEDGFNLTTSVSMMLFDTFLYGVMTWYIEAVFPGQYGI
PRPWYFPCTKSYWFGEESDEKSHPGSNQKRISEICMEEEPTHLKLGVSIQNLVKVYRDGMKVAVDGLALNF
YEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYILGKDIRSEMSTIRQNLGVCPQHNVLFDMLTVEEHI
WFYARLKGLSEKHVKAEMEQMALDVGLPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDP
YSRRGIWELLLKYRQGRTIILSTHHMDEADVLGDRIAIISHGKLCCVGSSLFLKNQLGTGYYLTLVKKDVE
SSLSSCRNSSSTVSYLKKEDSVSQSSSDAGLGSDHESDTLTIDVSAISNLIRKHVSEARLVEDIGHELTYV
LPYEAAKEGAFVELFHEIDDRLSDLGISSYGISETTLEEIFLKVAEESGVDAETSDGTLPARRNRRAFGDK
QSCLRPFTEDDAADPNDSDIDPESRETDLLSGMDGKGSYQVKGWKLTQQQFVALLWKRLLIARRSRKGFFA
QIVLPAVFVCIALVFSLIVPPFGKYPSLELQPWMYNEQYTFVSNDAPEDTGTLELLNALTKDPGFGTRCME
GNPIPDTPCQAGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKQ
NTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQEVNDAIKQMKKHL
KLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVINNAILRANLQKGENPSHYGITAFN
HPLNLTKQQLSEVALMTTSVDVLVSICVIFAMSFVPASFVVFLIQERVSKAKHLQFISGVKPVIYWLSNFV
WDMCNYVVPATLVIIIFICFQQKSYVSSTNLPVLALLLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNL
FIGINGSVATFVLELFTDNKLNNINDILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSW
DLVGRNLFAMAVEGVVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGGGQNDILEIKEL
TKIYRRKRKPAVDRICVGIPPGECFGLLGVNGAGKSSTFKMLTGDTTVTRGDAFLNKNSILSNIHEVHQNM
GYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVGEWAIRKLGLVKYGEKYAGNYSGGNKRKLSTAMAL
IGGPPVVFLDEPTTGMDPKARRFLWNCALSVVKEGRSVVLTSHSMEECEALCTRMAIMVNGRFRCLGSVQH
LKNRFGDGYTIVVRIAGSNPDLKPVQDFFGLAFPGSVLKEKHRNMLQYQLPSSLSSLARIFSILSQSKKRL
HIEDYSVSQTTLDQVFVNFAKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV*

Fig. 9A

SEQ ID NO: 2

GTCCCTGCTGTGAGCTCTGGCCGCTGCCTTCCAGGGCTCCCGAGCCACACGCTGGGGGTG
CTGGCTGAGGGAACATGGCTTGTTGGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCA
CTTTCAGAAGAAGACAAACATGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCT
TCCTGATCCTGATCTCTGTTCGGCTGAGCTACCCACCCTATGAACAACATGAATGCCATT
TTCCAAATAAAGCCATGCCCTCTGCAGGAACACTTCCTTGGGTTCAGGGGATTATCTGTA
ATGCCAACAACCCCCTGTTTCCGTTACCCGACTCCTGGGGAGGCTCCCGGAGTTGTTGGAA
ACTTTAACAAATCCATTGTGGCTCGCCTGTTCTCAGATGCTCGGAGGCTTCTTTTATACA
GCCAGAAAGACACCAGCATGAAGGACATGCGCAAAGTTCTGAGAACATTACAGCAGATCA
AGAAATCCAGCTCAAACTTGAAGCTTCAAGATTTCCTGGTGGACAATGAAACCTTCTCTG
GGTTCCTGTATCACAACCTCTCTCTCCCAAAGTCTACTGTGGACAAGATGCTGAGGGCTG
ATGTCATTCTCCACAAGGTATTTTTGCAAGGCTACCAGTTACATTTGACAAGTCTGTGCA
ATGGATCAAAATCAGAAGAGATGATTCAACTTGGTGACCAAGAAGTTTCTGAGCTTTGTG
GCCTACCAAGGGAGAAACTGGCTGCAGCAGAGCGAGTACTTCGTTCCAACATGGACATCC
TGAAGCCAATCCTGAGAACACTAAACTCTACATCTCCCTTCCCGAGCAAGGAGCTGGCTG
AAGCCACAAAAACATTGCTGCATAGTCTTGGGACTCTGGCCCAGGAGCTGTTCAGCATGA
GAAGCTGGAGTGACATGCGACAGGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCT
CCTCCACCCAAATCTACCAGGCTGTGTCTCGTATTGTCTGCGGGCATCCCGAGGGAGGGG
GGCTGAAGATCAAGTCTCTCAACTGGTATGAGGACAACAACTACAAAGCCCTCTTTGGAG
GCAATGGCACTGAGGAAGATGCTGAAACCTTCTATGACAACTCTACAACTCCTTACTGCA
ATGATTTGATGAAGAATTTGGAGTCTAGTCCTCTTTCCCGCATTATCTGGAAAGCTCTGA
AGCCGCTGCTCGTTGGGAAGATCCTGTATACACCTGACACTCCAGCCACAAGGCAGGTCA
TGGCTGAGGTGAACAAGACCTTCCAGGAACTGGCTGTGTTCCATGATCTGGAAGGCATGT
GGGAGGAACTCAGCCCCAAGATCTGGACCTTCATGGAGAACAGCCAAGAAATGGACCTTG
TCCGGATGCTGTTGGACAGCAGGGACAATGACCACTTTTGGGAACAGCAGTTGGATGGCT
TAGATTGGACAGCCCAAGACATCGTGGCGTTTTTGGCCAAGCACCCAGAGGATGTCCAGT
CCAGTAATGGTTCTGTGTACACCTGGAGAGAAGCTTTCAACGAGACTAACCAGGCAATCC
GGACCATATCTCGCTTCATGGAGTGTGTCAACCTGAACAAGCTAGAACCCATAGCAACAG
AAGTCTGGCTCATCAACAAGTCCATGGAGCTGCTGGATGAGAGGAAGTTCTGGGCTGGTA
TTGTGTTCACTGGAATTACTCCAGGCAGCATTGAGCTGCCCCATCATGTCAAGTACAAGA
TCCGAATGGACATTGACAATGTGGAGAGGACAAATAAAATCAAGGATGGGTACTGGGACC
CTGGTCCTCGAGCTGACCCCTTTGAGGACATGCGGTACGTCTGGGGGGGCTTCGCCTACT
TGCAGGATGTGGTGGAGCAGGCAATCATCAGGGTGCTGACGGGCACCGAGAAGAAAACTG

Fig. 9B

GTGTCTATATGCAACAGATGCCCTATCCCTGTTACGTTGATGACATCTTTCTGCGGGTGA

TGAGCCGGTCAATGCCCCTCTTCATGACGCTGGCCTGGATTTACTCAGTGGCTGTGATCA

TCAAGGGCATCGTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCATGGGCC

TGGACAACAGCATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTTCTTGTGA

GCGCTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCA

GCGTGGTGTTTGTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCTTCCTGA

TTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCA

CGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCA

AGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCC

TTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCTGTGGAGG

AAGATGGCTTCAATCTCACCACTTCGGTCTCCATGATGCTGTTTGACACCTTCCTCTATG

GGGTGATGACCTGGTACATTGAGGCTGTCTTTCCAGGCCAGTACGGAATTCCCAGGCCCT

GGTATTTTCCTTGCACCAAGTCCTACTGGTTTGGCGAGGAAAGTGATGAGAAGAGCCACC

CTGGTTCCAACCAGAAGAGAATATCAGAAATCTGCATGGAGGAGGAACCCACCCACTTGA

AGCTGGGCGTGTCCATTCAGAACCTGGTAAAAGTCTACCGAGATGGGATGAAGGTGGCTG

TCGATGGCCTGGCACTGAATTTTTATGAGGGCCAGATCACCTCCTTCCTGGGCCACAATG

GAGCGGGGAAGACGACCACCATGTCAATCCTGACCGGGTTGTTCCCCCCGACCTCGGGCA

CCGCCTACATCCTGGGAAAAGACATTCGCTCTGAGATGAGCACCATCCGGCAGAACCTGG

GGGTCTGTCCCCAGCATAACGTGCTGTTTGACATGCTGACTGTCGAAGAACACATCTGGT

TCTATGCCCGCTTGAAAGGGCTCTCTGAGAAGCACGTGAAGGCGGAGATGGAGCAGATGG

CCCTGGATGTTGGTTTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTCAGGTG

GAATGCAGAGAAAGCTATCTGTGGCCTTGGCCTTTGTCGGGGGATCTAAGGTTGTCATTC

TGGATGAACCCACAGCTGGTGTGGACCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGC

TGAAATACCGACAAGGCCGCACCATTATTCTCTCTACACACCACATGGATGAAGCGGACG

TCCTGGGGGACAGGATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGTGGGCTCCTCCC

TGTTTCTGAAGAACCAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGG

AATCCTCCCTCAGTTCCTGCAGAAACAGTAGTAGCACTGTGTCATACCTGAAAAAGGAGG

ACAGTGTTTCTCAGAGCAGTTCTGATGCTGGCCTGGGCAGCGACCATGAGAGTGACACGC

TGACCATCGATGTCTCTGCTATCTCCAACCTCATCAGGAAGCATGTGTCTGAAGCCCGGC

TGGTGGAAGACATAGGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAGGAGG

GAGCCTTTGTGGAACTCTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTTCTA

GTTATGGCATCTCAGAGACGACCCTGGAAGAAATATTCCTCAAGGTGGCCGAAGAGAGTG

GGGTGGATGCTGAGACCTCAGATGGTACCTTGCCAGCAAGACGAAACAGGCGGGCCTTCG

GGGACAAGCAGAGCTGTCTTCGCCCGTTCACTGAAGATGATGCTGCTGATCCAAATGATT

Fig. 9C

CTGACATAGACCCAGAATCCAGAGAGACAGACTTGCTCAGTGGGATGGATGGCAAAGGGT

CCTACCAGGTGAAAGGCTGGAAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAGA

GACTGCTAATTGCCAGACGGAGTCGGAAAGGATTTTTTGCTCAGATTGTCTTGCCAGCTG

TGTTTGTCTGCATTGCCCTTGTGTTCAGCCTGATCGTGCCACCCTTTGGCAAGTACCCCA

GCCTGGAACTTCAGCCCTGGATGTACAACGAACAGTACACATTTGTCAGCAATGATGCTC

CTGAGGACACGGGAACCCTGGAACTCTTAAACGCCCTCACCAAAGACCCTGGCTTCGGGA

CCCGCTGTATGGAAGGAAACCCAATCCCAGACACGCCCTGCCAGGCAGGGGAGGAAGAGT

GGACCACTGCCCCAGTTCCCCAGACCATCATGGACCTCTTCCAGAATGGGAACTGGACAA

TGCAGAACCCTTCACCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCTG

TGTGTCCCCCAGGGGCAGGGGGGCTGCCTCCTCCACAAAGAAAACAAAACACTGCAGATA

TCCTTCAGGACCTGACAGGAAGAAACATTTCGGATTATCTGGTGAAGACGTATGTGCAGA

TCATAGCCAAAAGCTTAAAGAACAAGATCTGGGTGAATGAGTTTAGGTATGGCGGCTTTT

CCCTGGGTGTCAGTAATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGATGCCATCA

AACAAATGAAGAAACACCTAAAGCTGGCCAAGGACAGTTCTGCAGATCGATTTCTCAACA

GCTTGGGAAGATTTATGACAGGACTGGACACCAGAAATAATGTCAAGGTGTGGTTCAATA

ACAAGGGCTGGCATGCAATCAGCTCTTTCCTGAATGTCATCAACAATGCCATTCTCCGGG

CCAACCTGCAAAAGGGAGAGAACCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCC

TGAATCTCACCAAGCAGCAGCTCTCAGAGGTGGCTCTGATGACCACATCAGTGGATGTCC

TTGTGTCCATCTGTGTCATCTTTGCAATGTCCTTCGTCCCAGCCAGCTTTGTCGTATTCC

TGATCCAGGAGCGGGTCAGCAAAGCAAAACACCTGCAGTTCATCAGTGGAGTGAAGCCTG

TCATCTACTGGCTCTCTAATTTTGTCTGGGATATGTGCAATTACGTTGTCCCTGCCACAC

TGGTCATTATCATCTTCATCTGCTTCCAGCAGAAGTCCTATGTGTCCTCCACCAATCTGC

CTGTGCTAGCCCTTCTACTTTTGCTGTATGGGTGGTCAATCACACCTCTCATGTACCCAG

CCTCCTTTGTGTTCAAGATCCCCAGCACAGCCTATGTGGTGCTCACCAGCGTGAACCTCT

TCATTGGCATTAATGGCAGCGTGGCCACCTTTGTGCTGGAGCTGTTCACCGACAATAAGC

TGAATAATATCAATGATATCCTGAAGTCCGTGTTCTTGATCTTCCCACATTTTTGCCTGG

GACGAGGGCTCATCGACATGGTGAAAAACCAGGCAATGGCTGATGCCCTGGAAAGGTTTG

GGGAGAATCGCTTTGTGTCACCATTATCTTGGGACTTGGTGGGACGAAACCTCTTCGCCA

TGGCCGTGGAAGGGGTGGTGTTCTTCCTCATTACTGTTCTGATCCAGTACAGATTCTTCA

TCAGGCCCAGACCTGTAAATGCAAAGCTATCTCCTCTGAATGATGAAGATGAAGATGTGA

GGCGGGAAAGACAGAGAATTCTTGATGGTGGAGGCCAGAATGACATCTTAGAAATCAAGG

AGTTGACGAAGATATATAGAAGGAAGCGGAAGCCTGCTGTTGACAGGATTTGCGTGGGCA

TTCCTCCTGGTGAGTGCTTTGGGCTCCTGGGAGTTAATGGGGCTGGAAAATCATCAACTT

TCAAGATGTTAACAGGAGATACCACTGTTACCAGAGGAGATGCTTTCCTTAACAAAAATA

Fig. 9D

GTATCTTATCAAACATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATG
CCATCACAGAGCTGTTGACTGGGAGAGAACACGTGGAGTTCTTTGCCCTTTTGAGAGGAG
TCCCAGAGAAAGAAGTTGGCAAGGTTGGTGAGTGGGCGATTCGGAAACTGGGCCTCGTGA
AGTATGGAGAAAAATATGCTGGTAACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAG
CCATGGCTTTGATCGGCGGGCCTCCTGTGGTGTTTCTGGATGAACCCACCACAGGCATGG
ATCCCAAAGCCCGGCGGTTCTTGTGGAATTGTGCCCTAAGTGTTGTCAAGGAGGGGAGAT
CAGTAGTGCTTACATCTCATAGTATGGAAGAATGTGAAGCTCTTTGCACTAGGATGGCAA
TCATGGTCAATGGAAGGTTCAGGTGCCTTGGCAGTGTCCAGCATCTAAAAAATAGGTTTG
GAGATGGTTATACAATAGTTGTACGAATAGCAGGGTCCAACCCGGACCTGAAGCCTGTCC
AGGATTTCTTTGGACTTGCATTTCCTGGAAGTGTTCTAAAAGAGAAACACCGGAACATGC
TACAATACCAGCTTCCATCTTCATTATCTTCTCTGGCCAGGATATTCAGCATCCTCTCCC
AGAGCAAAAAGCGACTCCACATAGAAGACTACTCTGTTTCTCAGACAACACTTGACCAAG
TATTTGTGAACTTTGCCAAGGACCAAAGTGATGATGACCACTTAAAAGACCTCTCATTAC
ACAAAAACCAGACAGTAGTGGACGTTGCAGTTCTCACATCTTTTCTACAGGATGAGAAAG
TGAAAGAAAGCTATGTATGAAGAATCCTGTTCATACGGGGTGGCTGAAAGTAAAGAGGAA
CTAGACTTTCCTTTGCACCATGTGAAGTGTTGTGGAGAAAAGAGCCAGAAGTTGATGTGG
GAAGAAGTAAACTGGATACTGTACTGATACTATTCAATGCAATGCAATTCAATGCAATGA
AAACAAAATTCCATTACAGGGGCAGTGCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAG
TGAAAGACTTGAATTTAGTTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCAA
TGGACATATGGGTTTGAACTCACACTTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATT
GGGGTTGCAACAATAATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAA
GGTAATGCACATCCTCATTCACTAAGCCATGCCATGCCCAGGAGACTGGTTTCCCGGTGA
CACATCCATTGCTGGCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTT
TGAAGCACCATGGTGTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCA
ACATTGAATATCAGTTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCC
TCTGATAAGCTGTTCTGGTGGCAGTAACATGCAACAAAAATGTGGGTGTCTCCAGGCACG
GGAAACTTGGTTCCATTGTTATATTGTCCTATGCTTCGAGCCATGGGTCTACAGGGTCAT
CCTTATGAGACTCTTAAATATACTTAGATCCTGGTAAGAGGCAAAGAATCAACAGCCAAA
CTGCTGGGGCTGCAACTGCTGAAGCCAGGGCATGGGATTAAAGAGATTGTGCGTTCAAAC
CTAGGGAAGCCTGTGCCCATTTGTCCTGACTGTCTGCTAACATGGTACACTGCATCTCAA
GATGTTTATCTGACACAAGTGTATTATTTCTGGCTTTTTGAATTAATCTAGAAAATGAAA

Fig. 9E

	Exon (bp)	Forward Primer	SEQ ID No.	Reverse Primer	SEQ ID No.		Intron(kb)	Intron (kb)
exon 1	140	GGCTGGATTAGCAGTCCTCA	70	ATCCCCAACTCAAAACCACA	119	intron 1	> 6.413	> 6.4
exon 2	94	GGATTTCCCAGATCCCAGTG	71	AAGTCCAATTTAGCCCACGTT	120	intron 2	> 4.241	> 4.2
exon 3	142	GACAGACTTGGCATGAAGCA	72	CCAGCCATTCAAAATTCTCC	121	intron 3	>1.248 (1.6)	1.6
exon 4	119	GCACTTGGCAGTCACTTCTG	73	GGTGCAGGTCAATTTCCAAT	122	intron 4	>1.512	>1.5
exon 5	122	CGTTTCTCCACTGTCCCATT	74	CCCCTTCACCACCATTACAA	123	intron 5	>1.769 (3)	3
exon 6	177	ACTTCAAGGACCCAGCTTCC	75	TGTCCAAGGAAAAGCCTCAC	124	intron 6	>2.726 (10)	10
exon 7	93	TCGGTTTCTTGTTTGTTAAACTCA	76	AGGACCTCTTGCCAGACTCA	125	intron 7	4.957	5
exon 8	241	TCCCAAGGCTTTGAGATGAC	77	AGGAGATGACACAGGCCAAG	126	intron 8	> 2.311 (2.5)	2.5
exon 9	140	GGCTCCAAAGCCCTTGTAA	78	CGCACACCTCTGAAGCTACC	127	intron 9	0.332	0.3
exon 10	117	GCTGCTGTGATGGGGTATCT	79	ACCTCACTCACACCTGGGAA	128	intron 10	4.208	4.2
exon 11	198	TTTGTAAATTTTGTAGTGCTCCTCA	80	GCCTCCTGCCTGAACCTTAT	129	intron 11	0.747	0.7
exon 12	206	TAGTCAGCCCTTGCCTCCTA	81	CAAAATCATGACACCAAGTTGAG	130	intron 12	0.523	0.5
exon 13	177	AAAGGGGCTTGGTAAGGGTA	82	CATGCACATGCACACACATA	131	intron 13	1.787	1.8
exon 14	223	GATGTGGTGCTCCCTCTAGC	83	CCTTAGCCCGTGTTGAGCTA	132	intron 14	1.747	1.7
exon 15	222	CAAGTGAGTGCTTGGGATTG	84	TGCTTTTATTCAGGGACTCCA	133	intron 15	1.059	1.1
exon 16	205	GCAAATTCAAATTTCTCCAGG	85	CCCATGCACTGCAGAGATTC	134	intron 16	1.105	1.1
exon 17	114	TCAAGGAGGAAATGGACCTG	86	AAGGCAGGAGACATCGCTT	135	intron 17	1.798	1.8
exon 18	172	CTGAAAGTTCAAGCGCAGTG	87	GGGATCAGCATGGTTTCCTA	136	intron 18	0.99	1
exon 19	132	TGCAGACTGAATGGAGCATC	88	GCTTAAGTCCCACTCCTCCC	137	intron 19	1.307	1.3
exon 20	143	GCCAGGGGACACTGTATTCT	89	ATTTTCCTCCGCATGTGTGT	138	intron 20	0.204	0.2
exon 21	138	AGGTCCTCTGCCTTCACTCA	90	TCACAGAAGCCTAGCCATGA	139	intron 21	0.706	0.7
exon 22	221	CCAGTGCTTACCCCTGCTAA	91	AACAGAGCAGGGAGATGGTG	140	intron 22	>0.866 (1.7)	1.7
exon 23	73	CACACAACAGAGCTTCTTGGA	92	TCTGCACCTCTCCTCCTCTG	141	intron 23	0.986	1
exon 24	203	ACCTGGAACAGGTGTGGTGT	93	ACTGGGGCCAACATTAATCA	142	intron 24	1.668	1.7
exon 25	49	GGGCTAACATGCCACTCAGTA	94	CTTCCCCATCTGCAACAAAC	143	intron 25	0.196	0.2
exon 26	114	GTTTGTTGCAGATGGGGAAG	95	GCTAAAGGCCATCCAAAGAA	144	intron 26	1.396	1.4
exon 27	149	CACCAGAAGAAGGAGCATGG	96	TCAAGTGCATCTGGGCATAA	145	intron 27	1.649	1.6
exon 28	125	CTGGACTCGTAGGGATTTGC	97	TCTGAAGTCCATTCCCTTGG	146	intron 28	>0.728 (1.4)	1.4
exon 29	99	GCCTGTCACAGAGAAATGCTT	98	CAATGTGGCATGCAGTTGAT	147	intron 29	>2.589 (3)	3
exon 30	190	TTACGGAATGATCCTGTGCTC	99	GAAGCTACCAGCCCATCCT	148	intron 30	1.521	1.5
exon 31	95	AGTCAGGTTTCCGGTCACAC	100	CATTTCCCCCACTGTTTCAG	149	intron 31	>0.944 (\)	>0.9
exon 32	33	CCGTTCCTTATATCCTCAGGTG	101	CCAAGGCTTTCTTCAATCCA	150	intron 32	>1.062 (/ 6.5)	>1.0
exon 33	106	CCTTGTACACACTCGCACTGA	102	GATCCGTTTAACCTGCCAAC	151	intron 33	1.475	1.5
exon 34	75	TGTTGTCCACAGGTTCCAGA	103	ATGCCCCTGCCAACTTTAC	152	intron 34	0.522	0.5
exon 35	170	TGAGGTTTATGGGCATGGTT	104	CTCTGCAGCTGTTCCCCTAC	153	intron 35	1.228	1.2
exon 36	178	ATGTTTTTCCTTGGCTGTGC	105	TATCAATCCATGGCCCTGAC	154	intron 36	>1.898 (2)	2
exon 37	116	ATCTGCCCTTTCTTGTCTGA	106	AGAGTCCCTGCCCTCCTTCT	155	intron 37	0.112	0.1
exon 38	145	AGGGAGCTGCACAGTGGATA	107	AAGGCAGTCAGCAGTGTCAA	156	intron 38	1.545	1.5
exon 39	124	TCACTCCCATATTTCAGAACTTGA	108	GGGGAACATCCTGTGCTTAG	157	intron 39	1.087	1.1
exon 40	130	TGTTTATTGGAAGATCGGTGAA	109	CCATTGGTGAGTGTTTCCCT	158	intron 40	0.265	0.3
exon 41	121	CGTTAGAGACTGAATCTTTGTCCTG	110	AGTCAGCAAACTGCTGGGTT	159	intron 41	>0.622 (0.9)	0.9
exon 42	63	AGTCCTGCCTTCCACAGTTG	111	ATTGCTCCATCCTGGCATAA	160	intron 42	0.909	0.9
exon 43	107	GGTAGTTACGTGTTAGGGGCA	112	TCATGGATGATTTTATGTGCTTC	161	intron 43	2.355	2.4
exon 44	142	CAGGAACATTAGGCCAGATTG	113	GCGTGTGGAAAAGCCATAAG	162	intron 44	0.372	0.4
exon 45	135	CATGTATGTGTAGGACAGCATGA	114	GCCAATCATACAACAGCCCT	163	intron 45	>1.059 (1.3)	1.3
exon 46	104	CTGTTTCAAAGATGCTTCTGC	115	TGATCGCATATTCTACTTGGAAA	164	intron 46	0.483	0.5
exon 47	93	CCTAGGAAGCTGGAATGCTG	116	TCCCTTTATTTTAGAGGCACCA	165	intron 47	0.659	0.7
exon 48	244	GGGTTCCCAGGGTTCAGTAT	117	GATCAGGAATTCAAGCACCAA	166	intron 48	0.941	0.9
exon 49	295	CTTGACCTAATTTCAACATCTGG	118	TGGGTTCCATAATAGAGTTTCACA	167		>1.075	

Fig. 10

Errors in public sequence (differences between all samples and Genbank entry AJ012376.1):

Exon/Intron	Nucleotide#	Amino acid change		Sequence difference/context	SEQ ID NO:
2	T150C	no change	Public sequence:	TGTCAGCTGTTACTGGAAGTCG	168
	A152G		Correct sequence:	TGTCAGCTGCTGCTGGAAGTCG	169
7	C839T	no change	Public sequence:	AGGAGCTGGCCGAAGCCACAA	170
			Correct sequence:	AGGAGCTGGCTGAAGCCACAA	171
33	C4738T	T1495I	Public sequence:	AATGATGCCACCAAACAAATG	172
			Correct sequence:	AATGATGCCATCAAACAAATG	173
35	C5017T	P1588L	Public sequence:	GAGGTGGCTCCGATGACCACA	174
			Correct sequence:	GAGGTGGCTCTGATGACCACA	175
43	G5995A	R1914K	Public sequence:	TTCCTTAACAGAAATAGTATC	176
			Correct sequence:	TTCCTTAACAAAAATAGTATC	177
48	C6577T	P2108L	Public sequence:	GGAAGTGTTCCAAAAGAGAAA	178
			Correct sequence:	GGAAGTGTTCTAAAAGAGAAA	179
49	G6899A	not applicable	Public sequence:	AGTAAAGAGGGACTAGACTTT	180
			Correct sequence:	AGTAAAGAGGAACTAGACTTT	181
Mutations:					SEQ ID NO:
13	A1864G	Q597R	More common:	GCCTACTTGCAGGATGTGGTG	182
			Less common:	GCCTACTTGCGGGATGTGGTG	183
14	delta CTT 2151-3	deltaL693	More common:	CCTCATTCCTCTTCTTGTGAGCG	184
			Less common:	CCTCATTCCT/CTTGTGAGCG	185
15	G2385A	V771M	More common:	GCAGGACTACGTGGGCTTCAC	186
			Less common:	GCAGGACTACATGGGCTTCAC	187
18	C2799T	R909Stop	More common:	AAAAGTCTACCGAGATGGGAT	188
			Less common:	AAAAGTCTACTGAGATGGGAT	189
18	C2860T	T929I	More common:	GGCCAGATCACCTCCTTCCTG	190
			Less common:	GGCCAGATCATCTCCTTCCTG	191
22	T3346C	M1091T	More common:	ACACACCACATGGATGAAGCG	192
			Less common:	ACACACCACACGGATGAAGCG	193
Intron 24	(+1) G to C	Altered transcript	More common:	CCTGGAAGAAGTAAGTTAAGT	194
	splice donor site	length	Less common:	CCTGGAAGAACTAAGTTAAGT	195
30	T4503C	C1477R	More common:	GCTGCCTGTGTGTCCCCCAGG	196
			Less common:	GCTGCCTGTGCGTCCCCCAGG	197
35	GG 4956-57 to C	Frameshift	More common:	TAGCCATTATGGAATTACTGCT	198
		at aa1628	Less common:	TAGCCATTATCAATTACTGCT	199
41	delta AAGATG 5752-7	delta(E,D)1893-1894	More common:	GATGAAGATGAAGATGTGAGGCGGGA	200
			Less common:	GATGAAGATG/TGAGGCGGGA	201
48	C6504T	R2144Stop	More common:	AATAGTTGTACGAATAGCAGG	202
			Less common:	AATAGTTGTATGAATAGCAGG	203
Promoter Variants:					
Location	Position Relative to Xenon cDNA	Position Relative to SEQ ID NO: 14 Containing Exon 1			SEQ ID NO:
1	G57C	8216	More common:	ACACGCTGGGGGTGCTGGCTG	204
			Less common:	ACACGCTGGGCGTGCTGGCTG	205
5'	(-) 4 ins. G	8158	More common:	GACCAGCCACGGCGTCCCTG	206
			Less common:	GACCAGCCACGGGCGTCCCTG	207
5'	A (-) 380 G	7780	More common:	CATTTTCTTAGAAAAGAGAGGT	208
			Less common:	CATTTTCTTAGAGAAGAGAGGT	209
5'	A (-) 479 C	7681	More common:	GAAAATTAGTATGTAAGGAAG	210
			Less common:	GAAAATTAGTCTGTAAGGAAG	211
5'	A (-) 738 G	7422	More common:	CCTCCGCCTGCCAGGTTCAGCGATT	212
			Less common:	CCTCCGCCTGCCGGGTTCAGCGATT	213
5'	A (-) 1045 G	7115	More common:	TATGTGCTGACCATGGGAGCTTGTT	214
			Less common:	TATGTGCTGACCGTGGGAGCTTGTT	215
5'	A (-) 1113 G	7047	More common:	GTGACACCCAACGGAGTAGGG	216
			Less common:	GTGACACCCAGCGGAGTAGGG	217
5'	(-) 1181 ins. CCCT	6979	More common:	AGTATCCCT/TGTTCACGAGAA	218
			Less common:	AGTATCCCTCCCTTGTTCACGAGAA	219

Fig. 11

Polymorphisms: Exon/Intron	Nucleotide#	Amino acid change		Sequence difference/context	SEQ ID NO:
5	G548A	no change	More common:	CTGGGTTCCTGTATCACAAC[G]	220
			Less common:	CTGGGTTCCTATATCACAAC[T]	221
6	G730A	R219K	More common:	GGCCTACCAAGGGAGAAAC[G]	222
			Less common:	GGCCTACCAAAGGAGAAAC[A]	223
Intron 7	G (+) 2383 T	Not applicable	Allele 1:	TTTAAAGGGGGTGATTAGGA	224
			Allele 2:	TTTAAAGGGGTTGATTAGGA	225
Intron 7	G (+) 3035 T	Not applicable	Allele 1:	GAAGAAATTTGTTTTTTTTGAT	226
			Allele 2:	GAAGAAATTTTTTTTTTTTGAT	227
8	C1010T	no change	More common:	GCGGGCATCCCGAGGGAGGGG	228
			Less common:	GCGGGCATCCTGAGGGAGGGG	229
8	G1022A	no change	More common:	AGGGAGGGGGGCTGAAGA[C]CA	230
			Less common:	AGGGAGGGGGACTGAAGA[T]CA	231
Intron 9	(-) 42 ins. G	Not applicable	More common:	AGGAGCCAAACGCTCATTG[T]	232
			Less common:	AGGAGCCAAAGCGCTCATTG[T]	233
Intron 13	T (+) 24 A	Not applicable	More common:	AAGCCACTGTTTTTAACCAG[T]	234
			Less common:	AAGCCACTGTATTTAACCAG[T]	235
15	A2394C	T774P	More common:	CGTGGGCTTCACACTCAAGA[T]	236
			Less common:	CGTGGGCTTCCCACTCAAGA[T]	237
15	G2402C	K776N	More common:	TCACACTCAAGATCTTCGCTG	238
			Less common:	TCACACTCAACATCTTCGCTG	239
Intron 14	C (+) 16 T	Not applicable	Allele 1:	GCAGCCTCACCCGCTCTTCGG	240
			Allele 2:	GCAGCCTCACTCGCTCTTCGG	241
17	A2723G	I883M	Allele 1:	AGAAGAGAATATCAGAAA[T]T	242
			Allele 2:	AGAAGAGAATGTCAGAAA[T]T	243
Intron 17	C (+) 2000 G	Not applicable	Allele 1:	GCGCAGTGCCCTGTGTCC[T]A	244
			Allele 2:	GCGCAGTGCGCTGTGTCC[T]A	245
21	T3233G	no change	More common:	GATCTAAGGTTGTCATTC[T]G	246
			Less common:	GATCTAAGGTGGTCATTC[T]G	247
Intron 21	G (+) 118 T	Not applicable	Allele 1:	CTCTTCTGTTAGCACAGAA[G]AGA	248
			Allele 2:	CTCTTCTGTTATCACAGAA[G]AGA	249
Intron 21	A (+) 563 G	Not applicable	Allele 1:	CATTCTAGGGATCATAGCCA[T]	250
			Allele 2:	CATTCTAGGGGTCATAGCCA[T]	251
Intron 24	G (+) 321 T	Not applicable	Allele 1:	AAGTACAGTGGGAGGAACAG[C]G	252
			Allele 2:	AAGTACAGTGTGAGGAACAG[C]G	253
Intron 29	A (-) 624 G	Not applicable	Allele 1:	ATTCCTAAAAAATAGAAATGCA	254
			Allele 2:	ATTCCTAAAAAGTAGAAATGCA	255
Intron 31	T (+) 30 C	Not applicable	More common:	GGCCCCTGCCTTATTATTAC[T]	256
			Less common:	GGCCCCTGCCGTATTATTAC[T]	257
Intron 33	A (+) 732 G	Not applicable	Allele 1:	TGAGAGAATTACTTGAACCCGG	258
			Allele 2:	TGAGAGAATTGCTTGAACCCGG	259
Intron 33	C (+) 898 T	Not applicable	Allele 1:	TTTGCTGAAACAATCACTGAC	260
			Allele 2:	TTTGCTGAAATAATCACTGAC	261
Intron 34	C (+) 234 T	Not applicable	Allele 1:	AACCTCAGTTCCCTCATCTGTG	262
			Allele 2:	AACCTCAGTTTCCTCATCTGTG	263
34	G4834A	R1587K	More common:	CTGGACACCAGAAATAATGTC	264
			Less common:	CTGGACACCAAAAATAATGTC	265
37	C5266G	S1731C	More common:	TCCTATGTGTCCTCCACCAAT	266
			Less common:	TCCTATGTGTGCTCCACCAAT	267
Intron 43	T (+) 18 C	Not applicable	More common:	AAGAAGTGGCTTGTATTTTGC	268
			Less common:	AAGAAGTGGCCTGTATTTTGC	269
Intron 43	A (+) 1665 G	Not applicable	Allele 1:	AACTGATTTGATTGGTATAGCTG	270
			Allele 2:	AACTGATTTGGTTGGTATAGCTG	271
48	C6521T	no change	More common:	CAGGGTCCAACCCGGACCTGA	272
			Less common:	CAGGGTCCAATCCGGACCTGA	273
Intron 10	(+) 14 ins. T	Not applicable	More common:	GCGTCAGGGATGGGGACAG	284
			Less common:	GCGTCAGGGATTGGGGACAG	285
Exon 16	G2547A	V825I	More common:	CCACTTCGGTCTCCATG	286
			Less common:	CCACTTCGATCTCCATG	287
Polymorphism in an ABC1 BAC contig:					
This polymorphism is within approximately 200 kb of the ABC1 gene					SEQ ID NO:
	A or G	not applicable	Allele 1:	TTGGGAGGCTAAGGCAGGAGAA	274
			Allele 2:	TTGGGAGGCTGAGGCAGGAGAA	275

Fig. 11

SEQ ID NO: 14

Genomic contig containing ABC1 exon 1:

Underline = putitive promotor element

acctcttatagaatgatagaattcctctggaatgattggataacttcatttcatccttgacttttaccttggaggattt
cttacccctttggcttctcaaatttgactattaaaatgttgcctttaaaaataggaacacagtttcaggggggagtac
cagcccatgacccttctgcaaggccccctaactcaaggtagtttccctggaactgtggtttatggaatgtttcaggagt
gtgaggaggtataatttaaggctgtcctagcaaggataccccttaaggatagagggcccagtagcatctggaggccagaa
aagttaaactgaggcagtcagattagcttcaggctcaattaagctgatgggtcagcctgggagaaattgcaggatgact
ctcaatatcccctcccacccccacagcagccacgatctgtctgtctttaatcatgggtgcagtgaacctgttctttcca
ggtgtcttggccttcagtaaccttgttaggcttgtccctgaacgtggctaccgatccaaagacacatgatcagagaggc
aattagagaacagacctttttccaaagcaagcatgttctgttgggcttagaagtttcatgtcctaatattataggaccct
gtgcatctctctggagatgaggcacatgagtcatatctgtgattcttgcttttgtgtcaacatctcatgaataggcaat
cagagctttggcaccaatgtattttcagttcatatctgatgtagttaaatccacctcctgctttgtagtttactggcaa
gctgtttttgatataagacatctagaacactgtaaatatataacatttttatttgtctattatacctcaattacgaaaa
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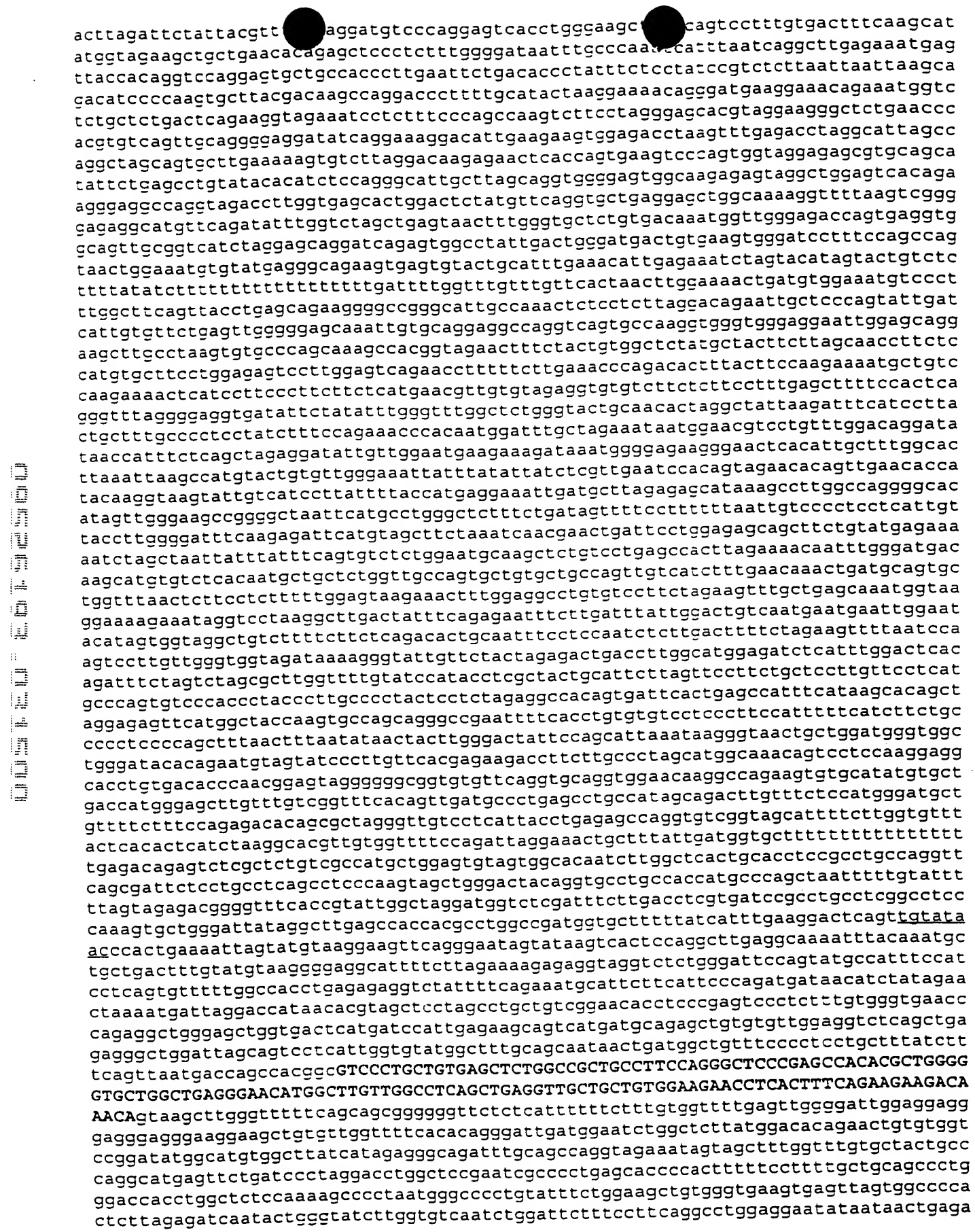

Fig. 12
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Date Printed: 03-04-2003

SEQ ID NO: 15

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Date Recue/Date Received 2020-05-29

SEQ ID NO: 16

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Fig. 12

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Date Recue/Date Received 2020-12-30

Fig. 12

SEQ ID NO: 17

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Confidential

SEQ ID NO: 18

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SEQ ID NO: 19

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SEQ ID NO: 20

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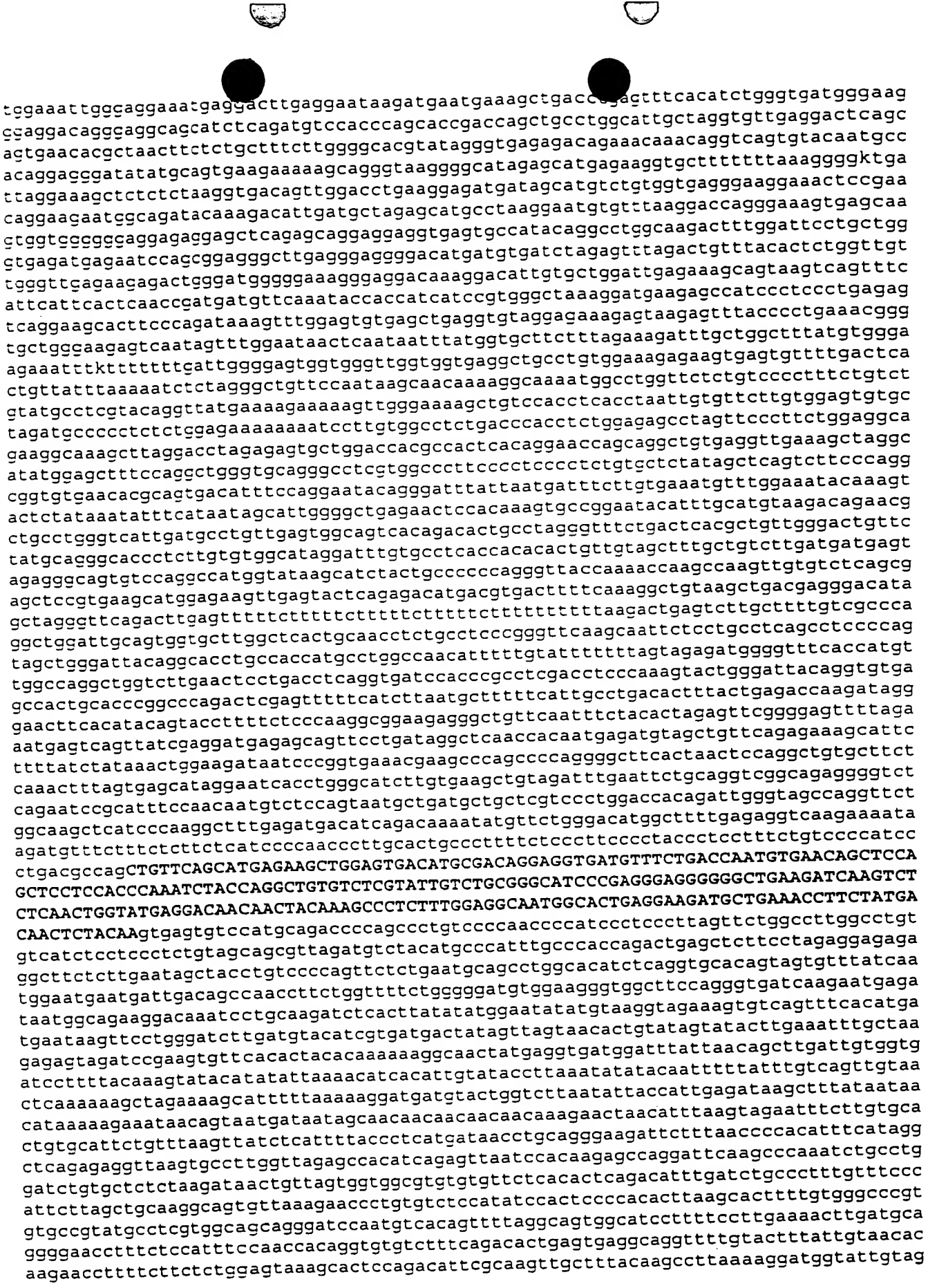
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Fig. 12

SEQ ID NO: 21

Genomic contig containing ABC1 exons 9 through 22:

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Confidential - Subject to Protective Order

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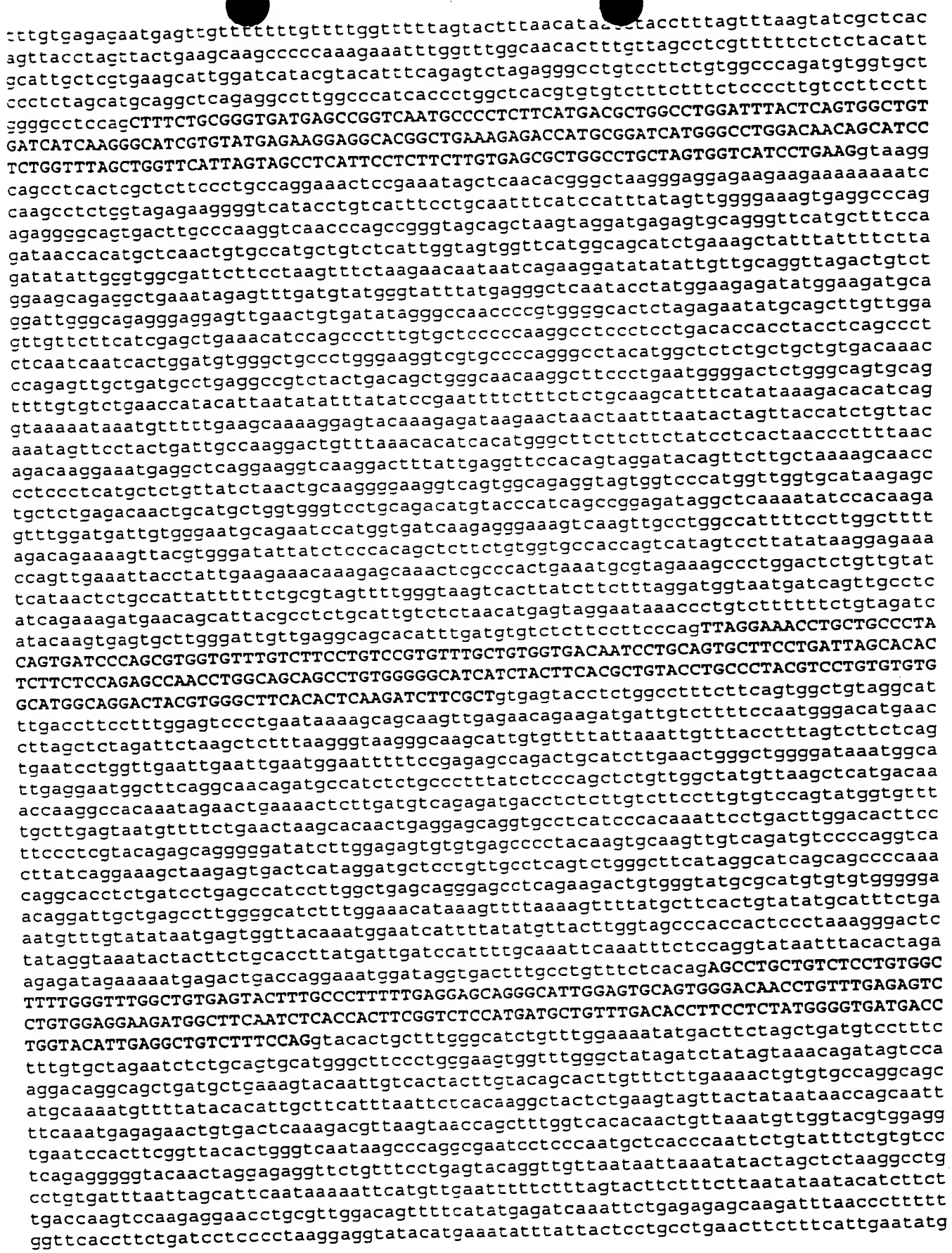
Fig. 12



Date Recue/Received Date 2005/12/15

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Fig. 12

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Fig. 12

SEQ ID NO: 22

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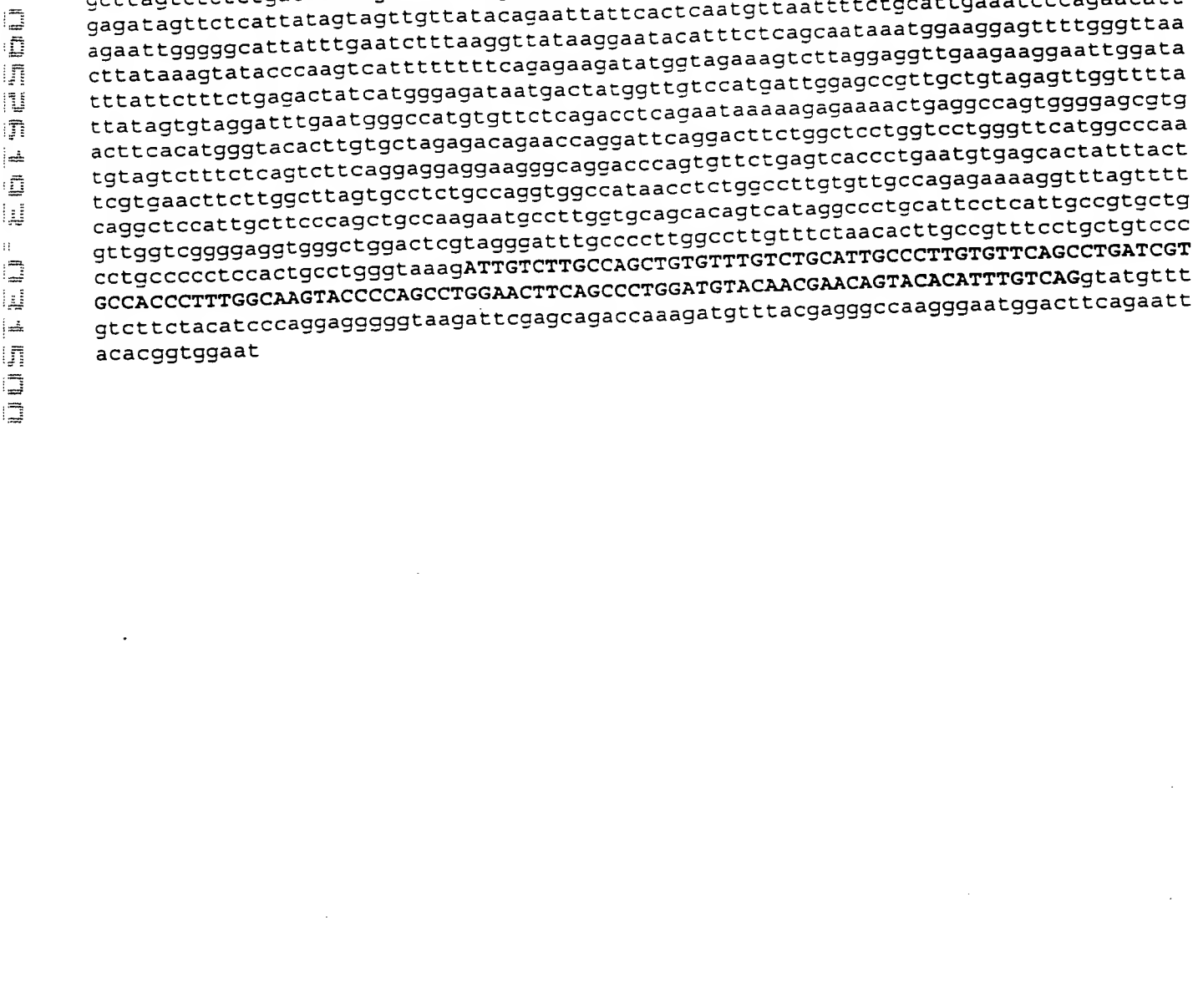
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SEQ ID NO: 23

Genomic contig conta[illegible] ABC1 exon 29:

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SEQ ID NO: 24

Genomic contig containing ABC1 exons 30 and 31:

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Confidential - Subject to Protective Order

SEQ ID NO: 25

Genomic contig containing ABC1 exon 32:_

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SEQ ID NO: 26

Genomic contig containing ABC1 exons 33 to 36:

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Fig. 12

SEQ ID NO: 27

Genomic contig conta[redacted]ng ABC1 exons 37 to 41:

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gatt

Date Recue/Date Received 2020-12-21

SEQ ID NO: 28

Genomic contig containing exons 42 through 45:

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DOCKET ALARM

SEQ ID NO: 29

Genomic contig containing ABC1 exons 46 to 49:

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GGATACTGTACTGATACTATTCAATGCAATGCAATTCAATGcaatgaaaacaaaattccattacaggggcagtgcctttg
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tgattttaaaatattaag

Fig. 12

DOSTEO - EP392500

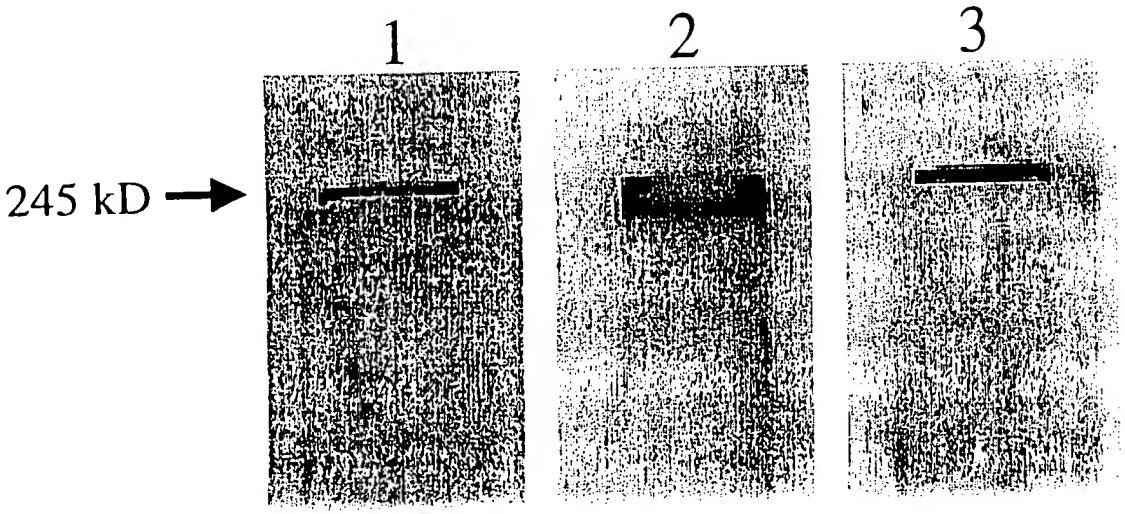

Fig. 13

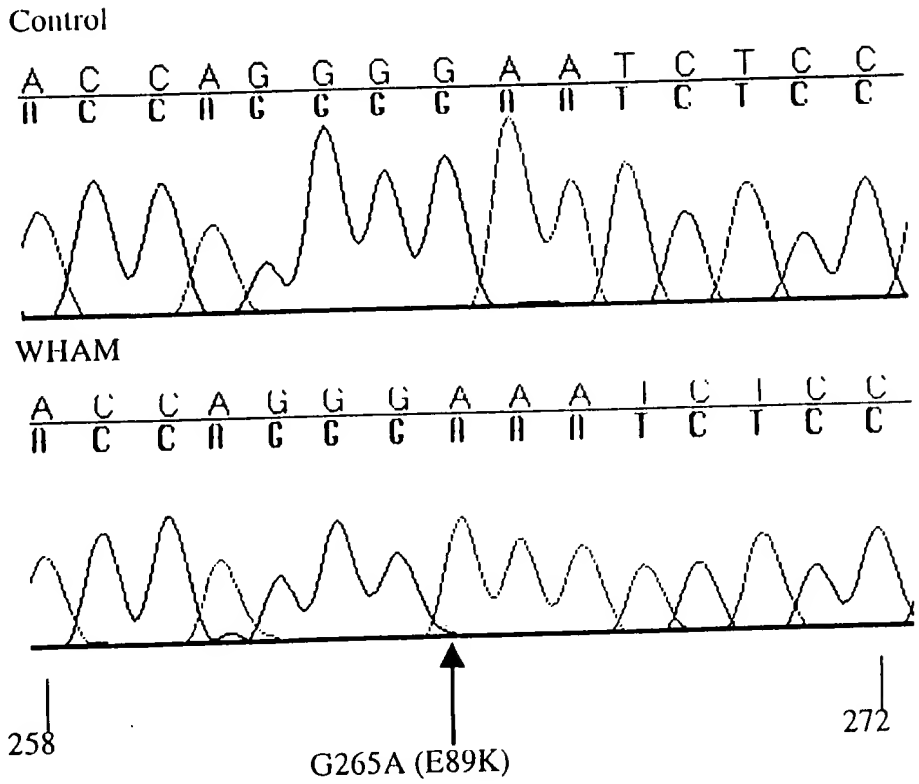
Control
A C C A G G G G A A T C T C C
WHAM
A C C A G G G A A A C C T C C
258
G265A (E89K)
272

Fig. 14

DOSTED: EP1925601

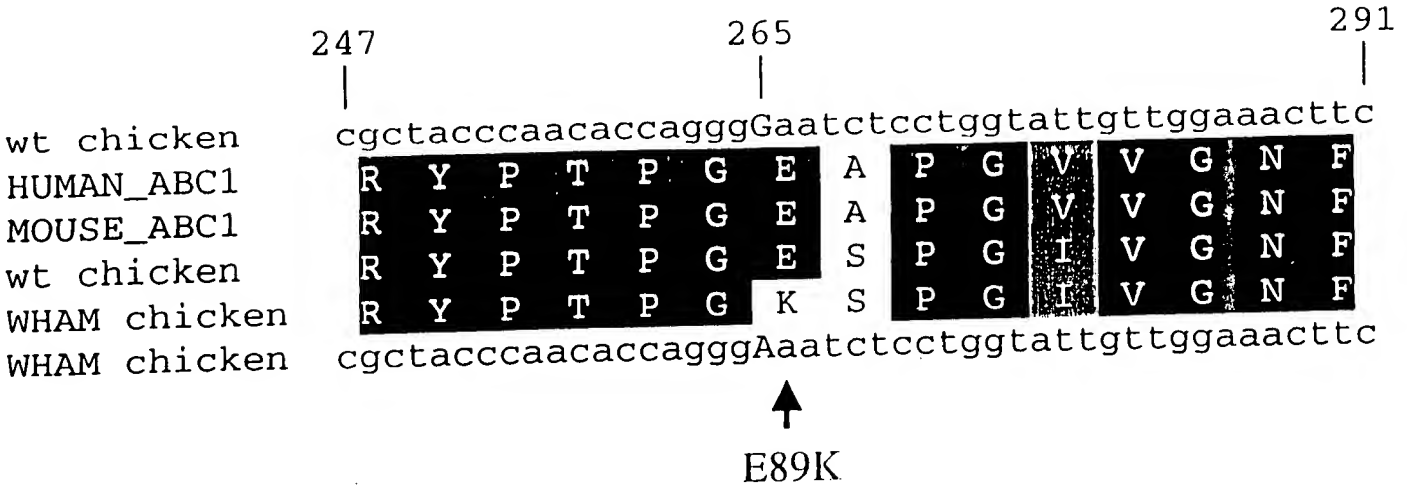

Fig. 15

No.	Name	Location in SEQ ID No. 14	Sequence	Sequence Length	Strand
1	PPRE	58-69	AGGTAAAAGTCA	12	Complement
2	PPRE	1997-2009	AGAGTAGAGGGCA	13	Lead
3	PPRE	2150-2161	ATGTCAAGTTCA	12	Lead
4	PPRE	2156-2169	AGTTCAAAAGGGCA	14	Lead
5	PPRE	4126-4139	AGGCCAGCAGGGCC	14	Complement
6	PPRE	5075-5087	AGGGCAGAAGTGA	13	Lead
7	PPRE	6604-6615	ATGCCAAGGTCA	12	Complement
8	PPRE	6731-6743	GGGGCAAGGGTA	13	Complement
9	PPRE	7220-7233	AGGTAATGAGGACA	14	Complement
10	PPRE	7554-7568	GGATCACGAGGTCA	15	Complement
1	SRE	159-166	CAGCCCAT	8	Lead
2	SRE	1133-1140	CAGCTCAC	8	Complement
3	SRE	1145-1152	CACACCAC	8	Lead
4	SRE	1809-1816	CAGCCCTC	8	Complement
5	SRE	1894-1901	CAGCCCAT	8	Lead
6	SRE	2563-2570	CAACCCAC	8	Lead
7	SRE	3303-3310	CAGCTCAC	8	Lead
8	SRE	3470-3477	CCGCCCAC	8	Lead
9	SRE	4784-4791	CTCCCCAC	8	Complement
10	SRE	4802-4809	CAGCCTAC	8	Complement
11	SRE	4970-4977	CACCTCAC	8	Complement
12	SRE	6487-6494	CAGCCTAC	8	Complement
13	SRE	6565-6572	CACCCAAC	8	Complement
14	SRE	6727-6734	CACCCTAC	8	Lead
15	SRE	7041-7048	CACCCAAC	8	Lead
16	SRE	8059-8066	CAGCCCTC	8	Complement
1	ROR(retinoic acid receptor related)	166-172	AGGGTCA	7	Complement
2	ROR(retinoic acid receptor related)	166-173	AAGGGTCA	8	Complement
3	ROR(retinoic acid receptor related)	363-370	ATGGGTCA	8	Lead
4	ROR(retinoic acid receptor related)	364-370	TGGGTCA	7	Lead
5	ROR(retinoic acid receptor related)	2218-2225	TAGGGTCA	8	Lead
6	ROR(retinoic acid receptor related)	2219-2225	AGGGTCA	7	Lead
7	ROR(retinoic acid receptor related)	3643-3649	TGGGTCA	7	Lead
8	ROR(retinoic acid receptor related)	6604-6610	AAGGTCA	7	Complement
1	SREBP-1 or "E box"	473-479	ACACCTG	7	Complement
2	SREBP-1 or "E box"	536-541	ACACATG	7	Lead
3	SREBP-1 or "E box"	537-543	TCATGTG	7	Complement
4	SREBP-1 or "E box"	555-661	TCATGTG	7	Complement
5	SREBP-1 or "E box"	925-931	ACACTTG	7	Lead
6	SREBP-1 or "E box"	967-973	TCACTTG	7	Lead
7	SREBP-1 or "E box"	968-974	TCAAGTG	7	Complement
8	SREBP-1 or "E box"	1063-1069	ACAGGTG	7	Complement
9	SREBP-1 or "E box"	1104-1110	TCACTTG	7	Lead
10	SREBP-1 or "E box"	1105-1111	TCAAGTG	7	Complement
11	SREBP-1 or "E box"	1561-1567	TCACTTG	7	Lead
12	SREBP-1 or "E box"	1670-1676	TCAAATG	7	Lead
13	SREBP-1 or "E box"	1748-1754	ACACTTG	7	Lead
14	SREBP-1 or "E box"	1749-1755	ACAAGTG	7	Complement
15	SREBP-1 or "E box"	1852-1858	TCATGTG	7	Lead
16	SREBP-1 or "E box"	1853-1859	ACACATG	7	Complement
17	SREBP-1 or "E box"	1899-1905	ACAAATG	7	Complement
18	SREBP-1 or "E box"	2199-2205	ACACGTG	7	Lead
19	SREBP-1 or "E box"	2393-2399	ACAGCTG	7	Complement
20	SREBP-1 or "E box"	2669-27005	ACACCTG	7	Lead
21	SREBP-1 or "E box"	2677-2683	TCACATG	7	Complement
22	SREBP-1 or "E box"	2740-2746	ACAACTG	7	Complement
23	SREBP-1 or "E box"	2969-2975	ACAAATG	7	Lead
24	SREBP-1 or "E box"	2979-2985	ACACATG	7	Lead
25	SREBP-1 or "E box"	2981-2987	ACATGTG	7	Lead
26	SREBP-1 or "E box"	2980-2986	ACATGTG	7	Complement
27	SREBP-1 or "E box"	2982-2988	ACACATG	7	Complement
28	SREBP-1 or "E box"	3461-3467	TCAGGTG	7	Lead
29	SREBP-1 or "E box"	3462-3468	TCACCTG	7	Complement
30	SREBP-1 or "E box"	3547-3553	TCAACTG	7	Complement
31	SREBP-1 or "E box"	3752-3758	ACACATG	7	Lead
32	SREBP-1 or "E box"	4226-4232	TCACCTG	7	Lead
33	SREBP-1 or "E box"	4582-4588	ACACGTG	7	Complement
34	SREBP-1 or "E box"	4588-4594	TCAGTTG	7	Lead
35	SREBP-1 or "E box"	4861-4867	TCAGGTG	7	Lead
36	SREBP-1 or "E box"	4951-4957	ACAAATG	7	Lead
37	SREBP-1 or "E box"	5096-5102	TCAAATG	7	Complement
38	SREBP-1 or "E box"	5912-5918	ACAGTTG	7	Lead
39	SREBP-1 or "E box"	5913-5919	TCAACTG	7	Complement
40	SREBP-1 or "E box"	6245-6251	ACACATG	7	Complement
41	SREBP-1 or "E box"	6288-6294	ACAACTG	7	Complement
42	SREBP-1 or "E box"	6623-6629	TCATTTG	7	Lead
43	SREBP-1 or "E box"	6836-6842	TCACCTG	7	Lead
44	SREBP-1 or "E box"	6837-6843	ACAGGTG	7	Complement
45	SREBP-1 or "E box"	7032-7038	ACAGGTG	7	Complement

Fig. 16

46	SREBP-1 or "E box"	7069-7075	TCAGGTG	7 Lead
47	SREBP-1 or "E box"	7101-7107	ACATATG	7 Complement
48	SREBP-1 or "E box"	7138-7144	ACAGTTG	7 Lead
49	SREBP-1 or "E box"	7139-7145	TCAACTG	7 Complement
50	SREBP-1 or "E box"	7240-7246	ACACCTG	7 Complement
51	SREBP-1 or "E box"	7467-7473	ACAGGTG	7 Lead
52	SREBP-1 or "E box"	7640-7646	TCATTTG	7 Lead
53	SREBP-1 or "E box"	7641-7647	TCAAATG	7 Complement
54	SREBP-1 or "E box"	7653-7659	TCAGTTG	7 Lead
55	SREBP-1 or "E box"	7654-7660	ACAACTG	7 Complement
56	SREBP-1 or "E box"	7735-7741	ACAAATG	7 Lead
57	SREBP-1 or "E box"	7838-7844	TCAGGTG	7 Complement
58	SREBP-1 or "E box"	7880-7886	TCATCTG	7 Complement
59	SREBP-1 or "E box"	8051-8057	TCAGCTG	7 Lead
60	SREBP-1 or "E box"	8052-8058	TCAGCTG	7 Complement

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Fig. 16